

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 05:02:30 ; Search time 1535.21 Seconds
(without alignments)
1170.088 Million cell updates/sec

Title: US-08-790-540A-1
Perfect score: 351
Sequence: 1 CAGGTGACGTGTTGGAGTC.....CTACAGTACTGTTTCTAGT 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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60: em_hg4.*
61: em_hg5.*
62: em_hg6.*
63: em_hg7.*
64: em_hum6.*
65: gb_hg18.*
66: gb_hg19.*
67: gb_hg20.*
68: gb_hg21.*
69: gb_hg22.*
70: gb_hg23.*
71: gb_vil.*
72: gb_vil2.*
73: gb_ba3.*
74: em_hg8.*
75: em_hg9.*
76: em_hg10.*
77: gb_pr6.*
78: gb_pr7.*
79: gb_sts1.*
80: gb_sts2.*
81: gb_pat1.*
82: gb_pat2.*
83: em_hg0.*
84: gb_hg24.*
85: gb_pr8.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	268.6	76.5	482	81	I08289	I08289 Sequence 6
2	268.6	76.5	488	11	S45356	S45356 Immunoglobulin
3	258.8	73.7	354	11	MUSIGMUD2A	M83724 Mouse monoclonal
4	257.4	73.3	413	81	A38870	A38870 Sequence 24
5	257.4	73.3	413	81	AR013776	AR013776 Sequence
6	257.4	73.3	721	81	AR027762	AR027762 Sequence
7	257.4	73.3	721	81	AR088763	AR088763 Sequence
8	257.4	73.3	733	81	AR027763	AR027763 Sequence
9	257.4	73.3	733	81	AR088764	AR088764 Sequence
10	254.8	72.6	348	11	MUSIGHVAB	L09000 Mus musculus
11	254.8	72.6	351	11	MUSIGHVACV	M34737 Mouse Ig H-chain
12	254.4	72.5	414	11	MMU62048	U62048 Mus musculus
13	254	72.4	354	11	AF113106	AF113106 Mus musculus
14	254	72.4	354	11	AF113107	AF113107 Mus musculus
15	254	72.4	354	11	AF113108	AF113108 Mus musculus
16	251.8	71.7	350	11	MUSIGHNRZ	M28187 Mus musculus
17	251.8	71.7	598	11	S55737	S55737 VH-immunoglobulin
18	251	71.5	351	21	E09589	E09589 cDNA encoding
19	250.2	71.3	637	11	S79401	S79401 VH183-DSP2
20	249.4	71.1	351	21	E09587	E09587 cDNA encoding
21	248.2	70.7	351	11	MUSIGVAAV	L08997 Mus musculus

22 248.2 70.7 420 11 AF045519 Mus muscu
23 248.2 70.7 420 11 AF045522 Mus muscu
24 246.8 70.3 348 12 AF112402 Synthetic
25 246.8 70.3 351 11 MMU293331 Mus muscu
26 246.6 70.3 354 11 MDIGNVBE
27 246.2 70.1 351 11 MDSIGVAU
28 246.2 70.1 480 11 MMRRK16V
29 246.2 70.1 1115 11 MMRRK16G
30 246 70.1 363 11 MDIGVAH
31 245.8 70.0 346 11 MMU55542
32 245.4 69.9 744 12 SCO250759
33 245.2 69.9 351 11 AF098319
34 245.2 69.9 351 11 AF163750
35 245.2 69.9 384 11 U01089
36 244.8 69.7 393 11 MMU02306
37 244.8 69.7 418 11 S67234
38 244.8 69.7 418 81 AR022586
39 244.8 69.7 418 81 AR037601
40 244.8 69.7 764 11 MDSIGHFAB1
41 244.4 69.6 729 5 AX011069
42 243.6 69.4 359 11 S71117
43 243.6 69.4 375 11 MNAHCVR15
44 243.4 69.3 420 11 AF045520
45 243.2 69.3 720 11 MMU40582

ALIGNMENTS

RESULT 1
LOCUS I08289 482 bp PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0380068.
ACCESSION I08289
VERSION I08289.1 GI:589001
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 482)
AUTHORS Zerler,B.D.
TITLE An expression system for production of chimeric monoclonal antibodies
JOURNAL Patent: EP 0380068-A1 6 01-AUG-1990;
FEATURES Location/Qualifiers
source 1..482
BASE COUNT 112 a 116 c 130 g 124 t
ORIGIN

Query Match 76.5%; Score 268.6; DB 81; Length 482;
Best Local Similarity 85.9%; Pred. No. 4.5e-77;
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAAGGTCCCTGAGACTCT 61
DB 133 AAGTCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAAGGTCCCTGAGACTCT 192
QY 62 CCGTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 121
DB 193 CCGTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 252
QY 122 CGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
DB 253 CGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 312
QY 182 TAGACACTGTGAGGCGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 241
DB 313 CAGACACTGTGAGGCGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 372
QY 242 TCCAAATGACTCTCTGAGACCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATACT 301

Db 373 TGCAAATGAGCAGTCTGAAGTCTGAGGACACAGCCGCTGATTACTGTGCAAGAAGGTACG 432
QY 302 ACGGAGTTTGGCTTACTTGGGCGCAAGGACTACAGTCACTGTTTCT 348
Db 433 CCTTCCCTTTTGGCTTACTTGGGCGCAAGGACTCTGGTCACTGTTCTCT 479
RESULT 2
LOCUS S45356 488 bp mRNA ROD 08-MAY-1993
DEFINITION immunoglobulin heavy chain variable-anti-human IL-2R [mice, mRNA
ACCESSION S45356
VERSION S45356.1 GI:2555660
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 488)
AUTHORS Rose,B., Gillespie,A., Wunderlich,D., Kelley,K., Dzuiba,J.,
Shedd,D., Cahill,K. and Zerler,B.
TITLE Differential effects of a murine and chimeric mouse/human
anti-interleukin-2 receptor antibody on human T-cell proliferation
JOURNAL Immunology 76 (3), 452-459 (1992)
MEDLINE 92406249
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 115041] from the original journal article.
This sequence comes from Fig. 1b.
FEATURES Location/Qualifiers
source 1..488
gene /organism="Mus sp."
80..487 /db_xref="taxon:10095"
CDS /partial
80..487 /gene="immunoglobulin heavy chain variable"
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/gene="immunoglobulin heavy chain variable"
/note="anti-human IL-2R; this sequence comes from Fig. 1b"
/codon_start=1
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/db_xref="GI:2555661"
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BASE COUNT 114 a 116 c 132 g 126 t
ORIGIN
Query Match 76.5%; Score 268.6; DB 11; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.5e-77;
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAAGGTCCCTGAGACTCT 61
DB 138 AAGTCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAAGGTCCCTGAGACTCT 197
QY 62 CCGTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 121
DB 198 CCGTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 257
QY 122 CGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
DB 258 CGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 317
QY 182 TAGACACTGTGAGGCGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 241
DB 318 CAGACACTGTGAGGCGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 377
QY 242 TGCAAATGACTCTCTGAGACCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATACT 301

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Db 378 TCGAATGACACTCTGAAGTCTGAGACACACGCCGTGTATTACTGTGCAAGAGTAGC 437
QY 302 ACGGCACTTTTGTCTACTGTGGGCAAGGACTACAGTGACTGTTCT 348
Db 438 GCCTCCCTTTTGTCTACTGTGGGCAAGGACTCTGGTCACTGTTCT 484

RESULT 3
LOCUS MUSTGM2A 354 bp mRNA ROD 08-MAY-2000
DEFINITION Mouse monoclonal antiidiotypic antibody IgM VDJ-region mRNA.
ACCESSION M83724
VERSION M83724.1 GI:197951
KEYWORDS D-region; Ig heavy chain; J-region; V-region; Immunoglobulin;
SOURCE immunoglobulin mu-chain; monoclonal antiidiotypic antibody.
ORGANISM house mouse.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE 1 (bases 1 to 354)
JOURNAL Taub, R., Hsu, J. C., Garsky, V. M., Hill, B. L., Erlanger, B. F. and
MEDLINE Kohn, L. D.
FEATURES peptide sequences from the hypervariable regions of two monoclonal
source anti-idiotypic antibodies against the thyrotropin (TSH) receptor
1 /organism="Mus musculus" are similar to TSH and inhibit TSH-increased cAMP production in
2 /db_xref="taxon:10090" FRTL-5 thyroid cells
3 /map="chromosome 6" J. Biol. Chem. 267 (9), 5977-5984 (1992)
4 /cell_line="4G11"
5 /tissue_type="hybridoma"
6 /gene="IgM"
7 /gene="IgM"
8 /codon_start=1
9 /product="immunoglobulin mu chain"
10 /protein_id="AA03040.1"
11 /db_xref="GI:197952"
12 /translation="EVQLVESGGGLVPGGSLKCAASGFTFSYAMSWVRSPEKR
13 LEWAEISSGGYTYPDVATGRFTISRDNKNTLYLEMSLRSEDTAMYCARDGIY
14 VFAYWGQTLTVSA"
15 V_region <1..294
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17 D_segment 295..309
18 /gene="IgM"
19 J_segment 310..354
20 /gene="IgM"
21 BASE COUNT 79 a 81 c 108 g 86 t
22 ORIGIN

Query Match 73.7%; Score 258.8; DB 11; Length 354;
Best Local Similarity 85.7%; Pred. No. 7.2e-74;
Matches 300; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 61
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QY 62 CCTGTGCAGCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121
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QY 122 CGGGCAAGGCTGTGGAGTGGTGCAGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181
Db 122 CAGAGAAGGCTGTGGAGTGGTGCAGAAATAGTAGTGGTGGTGTAGTACACCTACTATC 181
QY 182 TAGACACTGTGACAGGCCGATTCCACCATCTCCAGAGACAAATAGTAAGAACACCCCTATACC 241
Db 182 TAGACACTGTGAGAGGCCCGATTCCACCATCTCCAGAGACAGTCCAGAGAACACCCCTATACC 303
QY 242 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
Db 242 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
QY 304 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 363
Db 304 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 363
QY 302 ACGGCACTTTTGTCTACTGTGGGCAAGGACTACAGTGACTGTTCT 348
Db 364 TAGTCCCGTTTGTCTACTGTGGGCAAGGACTCTGGTCCACCGTCTCT 410

RESULT 5
LOCUS AR013776
DEFINITION AR013776 413 bp DNA PAT 05-DEC-1998
ACCESSION AR013776
VERSION AR013776.1 GI:3971230
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Db 182 CAGACACTGTGACGGCGCGATTCCACCATCTCCAGAGACAAATAGTAAGAACACCCCTATACC 241
QY 242 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 298
Db 242 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
QY 299 ACTACGCGAGTTTGTCTACTGTGGGCAAGGACTACAGTGACTGTTCT 348
Db 302 ACTACGCGAGTTTGTCTACTGTGGGCAAGGACTCTGGTCACTGTTCT 351

RESULT 4
LOCUS A38870
DEFINITION A38870 413 bp DNA PAT 05-MAR-1997
ACCESSION A38870
VERSION A38870.1 GI:2295288
KEYWORDS unidentifed.
SOURCE unidentifed.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 413)
AUTHORS King, D. J., Agair, J. R. and Owens, R. J.
TITLE HUMANISED ANTIBODIES DIRECTED AGAINST A33 ANTIGEN
JOURNAL Patent: WO 9413805-A 24 23-JUN-1994;
CELLTECH LTD (GB)
COMMENT Other publication AU 5656894 940704
Other publication GB 2278357 941130
Other publication JP 7504334T 950518.
FEATURES Location/Qualifiers
source 1..413
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 88 a 99 c 118 g 108 t
ORIGIN

Query Match 73.3%; Score 257.4; DB 81; Length 413;
Best Local Similarity 83.9%; Pred. No. 2.1e-73;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 61
Db 64 AAGTGAAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 123
QY 62 CCTGTGCAGCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121
Db 124 CCTGTGCAGCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 183
QY 122 CGGGCAAGGCTGTGGAGTGGTGCAGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181
Db 184 CGGAGAAGGCTGTGGAGTGGTGCAGAACCATTAGTAGTGGTGGTGTAGTACACCTACTATT 243
QY 182 TAGACACTGTGACAGGCCGATTCCACCATCTCCAGAGACAAATAGTAAGAACACCCCTATACC 241
Db 244 TAGACAGTGTGAAGGCCCGATTCCACCATCTCCAGAGACAGTCCAGAGAACACCCCTATACC 303
QY 242 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
Db 304 TCGAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 363
QY 302 ACGGCACTTTTGTCTACTGTGGGCAAGGACTACAGTGACTGTTCT 348
Db 364 TAGTCCCGTTTGTCTACTGTGGGCAAGGACTCTGGTCCACCGTCTCT 410

RESULT 5
LOCUS AR013776
DEFINITION AR013776 413 bp DNA PAT 05-DEC-1998
ACCESSION AR013776
VERSION AR013776.1 GI:3971230
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KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hamann,P.Ross, Hanman,L., Hollander,I., Holcomb,R., Hallett,W.,
Tsou,H. and Weiss,M.J.
TITLE Conjugates of methyltrithio antitumor agents and intermediates for
their synthesis
JOURNAL Patent: US 5773001-A 56 30-JUN-1998;
FEATURES Location/Qualifiers
source
i. .413
BASE COUNT 88 a 100 c 117 g 108 t
ORIGIN

Query Match 73.3%; Score 257.4; DB 81; Length 413;
Best Local Similarity 83.9%; Pred. No. 2.1e-73;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGCGGTGTGTCAGCCTGGAAGGTCCTGAGACTCT 61
DB 64 AAGTGAAGCTGTGGAGTCTGGGGAGCGCTTAGTGAAGCTGGAGGTCCTGAAACTCT 123
QY 62 CCTGTGACGCTCTGATTACACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121
DB 124 CCGTGTGACGCTCTGATTGCGCTTCAGTACCTATGACATGCTTGGGTCGCCAGCTC 183
QY 122 CGGGCAAGGCTCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCCTACTATT 181
DB 184 CGGAGAAGGCTGGAGTGGGTGCGCAACCATAGTAGTGGTGGTGTAGCCTACTATT 243
QY 182 TAGACACTGTGAGCGCCGATTCACCATCTCCAGACACATAGTAGAAGACCCCTATACC 241
DB 244 TAGACAGTGTGAAGGCCCATTCACCATCTCCAGACAGTCCGAGAACCCCTATACC 303
QY 242 TGCATTAAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
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QY 302 AGCGAGTTTGTCTACTGGGCGCAAGGACTACAGTACTGTTTCT 348
DB 364 TAGTCCCGTTTGTCTACTGGGCGCAAGGACTGTGTCACCTCTCT 410

RESULT 6
AR027762
LOCUS AR027762 721 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5856456.
ACCESSION AR027762
VERSION AR027762.1 GI:5938582
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 721)
AUTHORS Whitlow,M.D. and Filpula,D.R.
TITLE Linker for linked fusion polypeptides
JOURNAL Patent: US 5856456-A 15 05-JAN-1999;
FEATURES Location/Qualifiers
source
i. .721
BASE COUNT 176 a 172 c 189 g 184 t
ORIGIN

Query Match 73.3%; Score 257.4; DB 81; Length 721;
Best Local Similarity 83.9%; Pred. No. 2.2e-73;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGCGGTGTGTCAGCCTGGAAGGTCCTGAGACTCT 61
DB 365 AAGTGAAGCTGTGGAGTCTGGGGAGCGCTTAGTGAAGCTGGAGGTCCTTGAACACTCT 424
QY 62 CCTGTGACGCTCTGATTACACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121
DB 425 CCGTGTGACGCTCTGATTGCGCTTCAGTACCTATGACATGCTTGGGTCGCCAGACTC 484
QY 122 CGGGCAAGGCTCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCCTACTATT 181
DB 485 CGGAGAAGGCTGTGGAGTGGGTGCGCAACCATAGTAGTGGTGGTGTAGCCTACTATT 544
QY 182 TAGACACTGTGAGCGCGGATTCACCATCTCCAGACACATAGTAGAAGACCCCTATACC 241
DB 545 TAGACAGTGTGAAGGCCGATTCACCATCTCCAGACAGTCCGAGAACCCCTATACC 604
QY 242 TGCATTAAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB 605 TGCATTAAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 664
QY 302 AGCGAGTTTGTCTACTGGGCGCAAGGACTACAGTACTGTTTCT 348
DB 665 TAGTCCCGTTTGTCTACTGGGCGCAAGGACTGTGTCACCTCTCT 711

DB 365 AAGTGAAGCTGTGGAGTCTGGGGAGCGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT 424
QY 62 CCGTGTGACGCTCTGATTACACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121
DB 425 CCGTGTGACGCTCTGATTGCGCTTCAGTACCTATGACATGCTTGGGTCGCCAGACTC 484
QY 122 CGGGCAAGGCTCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCCTACTATT 181
DB 485 CGGAGAAGGCTGTGGAGTGGGTGCGCAACCATAGTAGTGGTGGTGTAGCCTACTATT 544
QY 485 CGGAGAAGGCTGTGGAGTGGGTGCGCAACCATAGTAGTGGTGGTGTAGCCTACTATT 544
QY 182 TAGACACTGTGAGCGCGGATTCACCATCTCCAGACACATAGTAGAAGACCCCTATACC 241
DB 545 TAGACAGTGTGAAGGCCGATTCACCATCTCCAGACAGTCCGAGAACCCCTATACC 604
QY 242 TGCATTAAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB 605 TGCATTAAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 664
QY 302 AGCGAGTTTGTCTACTGGGCGCAAGGACTACAGTACTGTTTCT 348
DB 665 TAGTCCCGTTTGTCTACTGGGCGCAAGGACTGTGTCACCTCTCT 711

RESULT 7
AR088763
LOCUS AR088763 721 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 15 from patent US 5990275.
ACCESSION AR088763
VERSION AR088763.1 GI:10015526
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 721)
AUTHORS Whitlow,M.D. and Filpula,D.R.
TITLE Linker and linked fusion polypeptides
JOURNAL Patent: US 5990275-A 15 23-NOV-1999;
FEATURES Location/Qualifiers
source
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BASE COUNT 176 a 172 c 189 g 184 t
ORIGIN

Query Match 73.3%; Score 257.4; DB 81; Length 721;
Best Local Similarity 83.9%; Pred. No. 2.2e-73;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGCGGTGTGTCAGCCTGGAAGGTCCTGAGACTCT 61
DB 365 AAGTGAAGCTGTGGAGTCTGGGGAGCGCTTAGTGAAGCTGGAGGTCCTTGAACACTCT 424
QY 62 CCTGTGACGCTCTGATTACACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121
DB 425 CCGTGTGACGCTCTGATTGCGCTTCAGTACCTATGACATGCTTGGGTCGCCAGACTC 484
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QY	62	CTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGACATGTCTTGGGTTGCCAGGCTC	121						
Db	437	CCTGTGCAGCCTCTGGATTCCGCTTCAGTAGCTATGACATGTCTTGGGTTGCCAGACTC	496						
QY	122	CGGGCAAGGCTCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCACCCTACTATT	181						
Db	497	CGGAGAGAGGCTGGAGTGGGTGCGCAACCACTTAGTGTGGTGGTAGCTACTATT	556						
QY	182	TAGACACTGTGCAGGGCCGATTCCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC	241						
Db	557	TAGACACTGTGAAGGCCGATTCCACATCTCCAGAGACAGTGCAGGAAACACCCCTATACC	616						
QY	242	TGCAATAGACTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT	301						
Db	617	TGCAATAGACTCTCTGAGTCTGTAGGACACGCGCTTGTATTACTGTGCACCGACTACGG	676						
QY	302	ACGGCAGTTTGTCTACTGGGGCCAGGACTACAGTGACTGTCTTCT	348						
Db	677	TAGTCCCGTTTGTCTACTGGGGCCAGGACTCTGTCTACTGTCTCT	723						
RESULT	10								
MUSIGVABB		348 bp	mrna		ROD		27-APR-1993		
LOCUS		Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region							
DEFINITION		sequence.							
ACCESSION		L09000							
VERSION		L09000.1							
KEYWORDS		V-region; immunoglobulin V region; processed gene.							
SOURCE		Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.							
ORGANISM		Mus musculus							
REFERENCE		1 (bases 1 to 348)							
AUTHORS		Bloom,D.B., Davignon,J.-L., Retter,M.W., Shlomchik,M.J., Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.							
TITLE		V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr mice							
JOURNAL		J. Immunol. 150, 1591-1610 (1993)							
MEDLINE		93163585							
FEATURES		Location/Qualifiers							
source		1..348							
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		/strain="mrl/mp-lpr/lpr"							
		/db_xref="taxon:10090"							
		/cell_line="anti-Sm hybridoma 4D12"							
		/cell_type="B-cell"							
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BASE COUNT		80 a.	87 c	102 g	79 t				
ORIGIN									
Query Match		72.6%;	Score 254.8;	DB 11;	Length 348;				
Best Local Similarity		83.5%;	Pred. No. 1.5e-72;						
Matches	289;	Conservative	0;	Mismatches	57;	Indels	0;	Gaps	0;
QY	2	AGGTGACGCTGTGGAGCTGTGGGGAGGCGTGTGAGCCTGGAAGTTCCTGAGACTCT	61						
Db	2	AAGTGAAGCTTGTGGAGCTGTGGGGAGCCTTAGTGAAGCCTGGAGGCTGCTGAACTCT	61						
QY	62	CTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGACATGTCTTGGGTTGCCAGGCTC	121						
Db	62	CTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGACATGTCTTGGGTTGCCAGACTC	121						
QY	122	CGGGCAAGGCTCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT	181						

Db 122 CGGCAAGAGCTCGAGTGGGTCTGAACCAATTAGTAGTGTTGGTAGCACCTACTATC 181

QY 182 TAGACACTGTGCAGGCCGCGGATTCACCATTCCAGAGACAATAGTAAGAACCCTATAACC 241
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Db 182 CAGACAGTGTGAAGGCCGCGGATTCACCATTCCAGAGACAATGCCAAGNACACCTGTATC 241
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QY 242 TGCAAATGAACCTCTGTAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACAATACT 301
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Db 242 TGCAAATGAGCAGTCTGAGGTCTCAGGACACGGCCATGTATTACTGTGCAAGACGAGTT 301
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QY 302 ACGCAGTTTTGCTTACTGGGCCAAGGGACTACAGTCACTGTTTC 347
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Db 302 ACTCCCTATGACTACTGGGGTCAAGSAACCTCAGTCACCGTCTC 347
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RESULT 11

MUSIGHACV 351 bp mRNA ROD 27-APR-1993

LOCUS Mouse Ig H-chain mRNA VDJ-region, partial cds.

DEFINITION M34737

ACCESSION M34737.1 GI:194750

VERSION D-region; J-region; V-region; immunoglobulin heavy chain; processed gene.

KEYWORDS Mouse (strain BALB/c) adult spleen anti-HA hybridoma H35-DI, cDNA to mRNA.

SOURCE Mus musculus

ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 351)

AUTHORS Clarke,S.H., Staudt,L.M., Kavaler,J., Schwartz,D., Gerhard,W.U. and Weigert,M.G.

TITLE V region gene usage and somatic mutation in the primary and secondary responses to influenza virus hemagglutinin

JOURNAL J..Immunol. 144, 2795-2801 (1990)

MEDLINE 90203619

FEATURES Location/Qualifiers

source 1..351

CDS /organism="Mus musculus"

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/note="Ig H-chain VDJ-region"

/codon_start=1

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BASE COUNT 89 a 82 c .99 g 81 t

ORIGIN

Query Match 72.6%; Score 254.8; DB 11; Length 351;

Best Local Similarity 83.5%; Pred. No. 1.5e-72;

Matches 289; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Db 2 AAGTGCAGCTGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAACTCT 61
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QY 62 CCTGTGAGCCTCTGGATTCACTTACCTAGTAGCTATGATGCTCTTGGGTTCCGCCAGCTC 121
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Db 62 CCTGTGAGCCTCTGGATTCACTTTCAGTGACTATTACATGCTATTGGTGTCCGCCAGACTC 121
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QY 122 CGGCAAGGGTCTGGAGTGGGTCCGAAGTTAGTAGTGTTGGTAGCACCTACTATT 181
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Db 122 CGAAAAAGAGCTGGAGTGGGTCTGCAACCATTAGTGATGGTGGTAGTACACTACTATC 181
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QY 182 TAGACACTGTGCAGGCCGCGGATTCACCATTCCAGAGACAATAGTAAGAACCCTATAACC 241
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Db 182 CAGACAGTGTGAAGGCCGCGGATTCACCATTCCAGAGACAATGCCAAGNACACCTGTATC 241
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QY 242 TGCAAATGAACCTCTGTAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACAATACT 301
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Db 242 TCGAAATAGCAGTCTGAAGTCTGAGGACACAGCCATTACTGTGCAGGATTACT 301

Qy 302 ACGCAGTTTTTCCTTACTGGGGCCCAAGGACTACAGTGACTTTTC 347
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Db 302 ACGTAGATGACTACTGGGGCCCAAGGCCACCCTCACAGTCTC 347
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RESULT 12
MMU62048 414 bp mRNA ROD 19-FEB-1997
DEFINITION Mus musculus polyreactive autoantibody, immunoglobulin IgM heavy chain mRNA, partial cds.
ACCESSION U62048
VERSION U62048.1 GI:1438576
KEYWORDS house mouse.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 414)
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and Dighiero,G.
TITLE Structural and affinity studies of IgM polyreactive natural autoantibodies
J. Immunol. 158 (2), 968-976 (1997)
97146071
REFERENCE 2 (bases 1 to 414)
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and Dighiero,G.
Direct Submission
Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France
FEATURES source
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:/strain="(CBA/NxBALB/c)F1"
:/db_xref="taxon:10090"
:/sex="female"
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CDS
BASE COUNT 88 a 110 c 115 g 101 t
ORIGIN

Query Match 72.5%; Score 254.4; DB 11; Length 414;
Best Local Similarity 84.6%; Pred No. 2e-72;
Matches 301; Conservative 0; Mismatches 46; Indels 9; Gaps 1;

Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGTGTGCAGCCCTGGAAGTCTCCTGAGACTCT 61
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Qy 62 CTTGTGCAGCTCTGGATTTCACCTTCAGTACTATGACATCTCTGGGTTCGCCAGGCTC 121
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Qy 122 CGGGCAAGGGTCTGGAGTGGGTGCGAAAAGTTAGTGTGGTGGTGGTAGCACCCTACTATT 181
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Db 122 CGGAGAAGAGCTGGAGTGGGTGCGAACCATTAAGTAGTGGTGGTAGTTACACTACTATC 181
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Qy 182 TAGACACTGTGCAGGCGCGGATTCACCATCTCCAGAGACAANTAGTAAGAACACCCCTATACC 241
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Db 182 CAGACAGTGTGAAGGGGGGATTCACCATCTCCAGAGACAANTAGTAAGAACACCCCTGTACC 241
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Qy	242	TGCAATGAAC	CTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAGACATAACT	301
Db	242	TGCAATGAC	CAGTCTGAGCTGTGAGGACACAGCCTTGTATTACTGTGCAAGAGTTACT	301
Qy	302	ACGG--	CACTTTTGCTACTGGGCCAAGGACTACAGTGACTGTTCT	348
Db	302	ATAGTAAC	TCTTTGCTTACTGGGCCAAGGACTCGGTCACGTCTCT	351
RESULT 14				
AF113107				
LOCUS	AF113107	354 bp	mrna	21-SEP-2000
DEFINITION	Mus musculus hybridoma Y6-8G3 anti-myeolperoxidase immunoglobulin heavy chain variable region mRNA, partial cds.			
ACCESSION	AF113107			
VERSION	AF113107.1 GI:4768654			
KEYWORDS				
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Jethwa,H.S., Clarke,S.H., Itoh-Lindstrom,Y., Falk,R.J., Jennette,J.C. and Nachman,P.H.			
TITLE	Restriction in V kappa gene use and antigen selection in anti-myeolperoxidase response in mice			
JOURNAL	J. Immunol. 165, 3890-3897 (2000)			
REFERENCE	2 (bases 1 to 354)			
AUTHORS	Jethwa,H.S., Nachman,P.H., Jennette,J.C., Falk,R.J., Kinjoh,K., Tuttle,K. and Taylor,J.			
TITLE	Direct Submission			
JOURNAL	Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525, Chapel Hill, NC 27599, USA			
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CDS				
BASE COUNT	84	a	80	c
ORIGIN	102	g	88	t

[illegible]

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Db 302 ATAGTAACACTACTTTGCTTACTGGGCCCAAGGACACAGTACTGTTTCT 351
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

RESULT 15
AF113108 354 bp mRNA ROD 21-SEP-2000
LOCUS Mus musculus hybridoma Y6-9G3 anti-myeloperoxidase immunoglobulin
DEFINITION heavy chain variable region mRNA, partial cds.
ACCESSION AF113108
VERSION AF113108.1 GI:4768656
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Jethwa,H.S., Clarke,S.H., Itoh-Lindstrom,Y., Falk,R.J.,
Jennette,J.C. and Nachman,P.H.
TITLE Restriction in V kappa gene use and antigen selection in
anti-myeloperoxidase response in mice
J. Immunol. 165, 3890-3897 (2000)
JOURNAL
AUTHORS anti-myeloperoxidase response in mice
REFERENCE Jethwa,H.S., Nachman,P.H., Jennette,J.C., Falk,R.J., KinJoh,K.,
Tuttle,R. and Taylor,J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
FEATURES
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BASE COUNT 84 a 80 c 102 g 88 t
ORIGIN
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Query Match 72.4%; Score 254; DB 11; Length 354;
Best Local Similarity 84.9%; Pred. No. 2.7e-72;
Matches 297; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
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Qy 122 CGGCAAGGCTTGGAGTGGGTGCGAAAAGTTAGTGGTGGTAGCCACTACTATT 181
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Qy 182 TAGACACTGTGCAGGCGCGATCCACTCTCCAGAGACAATAGTAAGAACCCCTATACC 241
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Qy 242 TGCAATGAACCTCTGAGAGCCGAGGACACAGCCGTTGTTACTGTGCAAGACATAACT 301
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Job time: 15030 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 01:33:05 ; Search time 1450.07 Seconds
(without alignments)
1696.213 Million cell updates/sec

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Perfect score: 351
Sequence: 1 CAGGTCAGCTGTGGAGTC.....CTACAGTCACTGTTTCTAGT 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues 15983484
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	230.4	65.6	469	23	AI645111	AI645111 ms87g10.y
2	230.4	65.6	823	3	AA170256	AA170256 ms87g10.y
3	229.8	65.3	406	90	AW401971	AW401971 UI-HF-BKO
4	228.4	65.1	454	95	AW824857	AW824857 us08c01.y
5	226.8	64.6	440	90	AW408304	AW408304 UI-HF-BKO
6	226.6	64.4	511	90	AW402613	AW402613 UI-HF-BKO
7	224.6	64.0	548	90	AW408295	AW408295 UI-HF-BKO
8	223.8	63.9	436	90	AW402311	AW402311 UI-HF-BKO
9	223.4	63.6	456	90	AW403059	AW403059 UI-HF-BKO
10	218.8	62.3	412	90	AW402895	AW402895 UI-HF-BKO
11	218.2	62.2	487	90	AW403862	AW403862 UI-HF-BKO
12	217.8	62.1	471	90	AW403220	AW403220 UI-HF-BKO
13	217.6	62.0	483	90	AW403901	AW403901 UI-HF-BKO
14	217.2	61.8	491	90	AW402907	AW402907 UI-HF-BKO
15	216.2	61.6	518	90	AW402029	AW402029 UI-HF-BKO
16	215.8	61.5	390	93	AW631411	AW631411 hh85d05.y
17	215.6	61.4	361	90	AW403412	AW403412 UI-HF-BKO
18	215.4	61.4	536	90	AW402624	AW402624 UI-HF-BKO
19	214.8	61.2	447	90	AW402793	AW402793 UI-HF-BKO
20	214.6	61.1	372	9	AA581192	AA581192 nd38b11.r
21	214.6	61.1	582	90	AW401386	AW401386 UI-HF-BKO
22	214.6	61.0	503	90	AW402572	AW402572 UI-HF-BKO
23	214.6	61.0	516	90	AW401728	AW401728 UI-HF-BKO
24	213.8	60.9	406	90	AW403983	AW403983 UI-HF-BKO
25	213.6	60.9	397	90	AW403886	AW403886 UI-HF-BKO
26	211.6	60.3	475	90	AW402740	AW402740 UI-HF-BKO
27	211.2	60.2	510	90	AW403707	AW403707 UI-HF-BKO
28	210.6	60.0	396	90	AW407843	AW407843 UI-HF-BKO
29	209.9	59.5	413	90	AW402865	AW402865 UI-HF-BKO
30	208.2	59.3	411	90	AW403298	AW403298 UI-HF-BKO
31	207.8	59.2	484	90	AW401679	AW401679 UI-HF-BKO
32	207.6	59.1	553	90	AW401769	AW401769 UI-HF-BKO
33	206.6	58.9	443	90	AW401428	AW401428 UI-HF-BKO
34	206.4	58.8	445	90	AW408316	AW408316 UI-HF-BKO
35	206.4	58.7	511	90	AW402453	AW402453 UI-HF-BKO
36	205.8	58.6	378	11	AA740786	AA740786 OD32611.s
37	205.8	58.6	669	158	AA740786	AA740786 OD32611.s
38	205.6	58.6	459	90	AW402542	AW402542 UI-HF-BKO
39	205.4	58.5	434	93	AW630702	AW630702 hh86d11.y
40	204.8	58.3	677	106	BE286624	BE286624 601090210
41	204.6	58.3	367	90	AW408326	AW408326 UI-HF-BKO
42	204.4	58.2	405	90	AW402449	AW402449 UI-HF-BKO
43	203.4	57.9	447	90	AW403163	AW403163 UI-HF-BKO
44	203.4	57.8	412	95	AW800162	AW800162 MR2-UM006
45	202.4	57.7	331	90	AW402553	AW402553 UI-HF-BKO

ALIGNMENTS

RESULT 1
AI645111
LOCUS
DEFINITION
AI645111
ACCESION
VERSION

AI645111 469 bp mRNA EST
ms87g10.y1 Soares mouse 3Nbms Mus musculus cDNA clone IMAGE:618594
5' similar to gb:xl4584 IG HEAVY CHAIN PRECURSOR V-III REGION
(HUMAN); gb:U23089 Mus musculus CBI7 SCID immunoglobulin heavy chain V region mRNA, (MOUSE); mRNA sequence.

AI645111.1 GI:4723586


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Db 179 CCTGTGCAGCCTCTGGATTCACTTTTCAGTAGTATGCCATGCTCTGGGTTGCCAGACTC 238
QY 122 CGGCAAGGGTCTGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCAGCCTACTATT 181
Db 239 CAGAGAAGAGGCTGGAGTGGGTGCGATACATAGTAGTGGTGGTATTACTACTATG 298
QY 182 TAGACACTGTGAGGCGCCATTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 299 CAGACACTGTGAGGCGCGATTCACCATCTCCAGAGACAATGCCAGGACACCCCTGTACC 358
QY 242 TCGAAATGAACCTCTCTGAGAGCGGAGGACACAGCCGCTGATTACTGTGCAAGACAT 297
Db 359 TCGAAATGAGCAGTCTGAGTCTGAGGACACAGCCATGATTACTGTACAAGAGAT 414

RESULT 3
AW401971 406 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BK0-aa0-C-04-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054342 5', mRNA sequence.
ACCESSION AW401971
VERSION AW401971.1 GI:6920657
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="vector: p7T3-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb), directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 89 a 93 c 123 g 100 t
ORIGIN
Query Match 65.5%; Score 229.8; DB 90; Length 406;
Best/Local Similarity 80.9%; Pred.No. 2.4e-59;
Matches 280; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGGTGTGCAGCCTGGAAGGTCCTGTGAGACTCT 61
Db 60 AGGTGCAGCTGTGGAGTCTGGGGAGCGTGTGTACAGCCTGGAGGTCCTGTGAGACTCT 119
QY 62 CCTGTGCAGCCTCTGGATTCACTTTTCAGTAGTATGCCATGCTCTGGGTTGCCAGGCTC 121
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Db 120 CCTGTGCAGCCTCTGGATTCACTTTTCAGTAGTATGAAATGAAGTGGTCCGCCAGGCTC 179
QY 122 CGGCAAGGGTCTGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCAGCCTACTATT 181
Db 180 CAGGAAGGGCTGGAGTGGGTTCATACATAGTAGTAGTGGTAGTACCATATACTACG 239
QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 240 CAGACTCTGTGAAGGCGGATTCACCATCTCCAGAGACAACGCCNAGAACCTCACTGTATC 299
QY 242 TCGAAATGAATCTCTGAGAGCCGAGGACACAGCGGTGATTACTGTGCAGACATACT 301
Db 300 TCGAAATGAACAGCTGTGAGAGCCGAGGACACGCTGTTTATTACTGTGCGAGTCAATATA 359
QY 302 ACGGAGCTTTGCTTACTGGGCGCAAGGACTACAGTCTGACTGTTTC 347
Db 360 ACAACAGCT---GGTACTGGGCGCAGGGAACCCCTGGTCACCGCTCTC 402

RESULT 4
AW824857 454 bp mRNA EST 17-MAY-2000
LOCUS us08c01.y1 Soares_NMGBC_B-cell Mus musculus cDNA clone
DEFINITION IMAGE:3136464 5' Similar to gb:U14584 IG HEAVY CHAIN PRECURSOR
V-III REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID
immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.
ACCESSION AW824857
VERSION AW824857.1 GI:7917934
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 454)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1061924
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 454
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/db_xref="taxon:10090"
/clone="IMAGE:3136464"
/clone_lib="Soares_NMGBC_B-cell"
/tissue_type="germinal B-cell from resting spleen"
/lab_host="DH10B (phage resistant)"
/note="vector: p7T3-Pac (Pharmacia) with a modified
polylinker; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGAGGATTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p7T3 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 102 a 109 c 127 g 116 t
ORIGIN
Query Match 65.1%; Score 228.4; DB 95; Length 454;
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Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

[illegible]

Db 426 GTTATCCACGGCGGCTTTGACTACTGGGCCAGGAAACCCGGTCCACCGTCTC 480

RESULT 8
AW402311
LOCUS
DEFINITION
16-FEB-2000
EST
15-FEB-2000
UI-HF-BK0-saj-h-04-0-UI.r1 NIH_MGC_36 Homo sapiens CDNA clone
IMAGE:3054175 5', mRNA sequence.
ACCESSION
AW402311
VERSION
AW402311.1
KEYWORDS
GI:6920997
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 436)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact::Robert Strausberg, Ph.D.
COMMENT
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1. .436
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.. /db_xref="taxon:9606"
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.. /tissue_type="lymph"
.. /cell_type="germinal center B cells"

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/pbrp/image/image.html

/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 89 a 109 c 136 g 102 t
ORIGIN

Query Match 63.8%; Score 223.8; DB 90; Length 436;
Best Local Similarity 79.3%; Pred. No. 1.6e-57;
Matches 280; Conservative 0; Mismatches 67; Indels 6; Gaps 1;
QY 1 CAGGTGACACTGGTGGAGCTGGGGAGGCGTGTGTCAGCCCTGGAGGTCCTCGAGACTC 60
DB 71 CAGGTGCAACTGGTGGAGCTGGGGAGGCGTGTGTCAGCCCTGGAGGTCCTCGAGACTC 130
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCT 120
DB 131 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCT 190
QY 121 CCGGCAAGGGCTGAGTGGGTCGCCAAGTAGTAGTGGTGGTAGCCTACTAT 180
DB 191 CCGGCAAGGGCTGAGTGGGTCGCCAAGTAGTAGTGGTGGTAGCCTACTAT 250
QY 181 TTAGACACTGTGAGGCGGATTCCACCTCTCCAGAGACAATAGTAAGAACACCCCTATAC 240
DB 251 GCAAACTCGTGAAGGCGATTCCACCTCTCCAGAGACAATAGTAAGAACACCGTGTAT 310
QY 241 CTGCAAAATGAATCTCTGAGAGCCGAGGACACAGCCGCTGTATTACTGTGTCAGA 294
DB 311 CTGCAATGAACAACCTCTGAGAGCCGAGGACAGGCTGTGTATTACTGTGCGGAGGGAGT 370
QY 295 CATACTAGGCAAGTTTCTTACTGGGCGCAAGGACTACAGTACTGTTTC 347
DB 371 GGGACCTGGGCGCACTTTGACTACTGGGCGCAGGAACCCCTGGTCACCGCTC 423

RESULT 9
AW403059 456 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BKO-aal-f-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054090 5', mRNA sequence.
ACCESSION AW403059
VERSION AW403059.1 GI:6921885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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1. 456
Location/Qualifiers
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/clone="IMAGE:3054090"

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/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 103 a 104 c 139 g 110 t
ORIGIN

Query Match 63.6%; Score 223.4; DB 90; Length 456;
Best Local Similarity 84.5%; Pred. No. 2.2e-57;
Matches 251; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 2 AGGTGCACCTGGTGGAGTCTGGGGAGGCGTGTGTCAGCCCTGGAGGTCCTCGAGACTCT 61
DB 110 AGGTGCACCTGGTGGAGTCTGGGGAGGCGTGTGTCAGCCCTGGAGGTCCTCGAGACTCT 169
QY 62 CCGTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCTC 121
DB 170 CCGTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCTC 229
QY 122 CCGGCAAGGGCTGAGTGGGTCGCCAAGTAGTAGTGGTGGTAGCCTACTATT 181
DB 230 CAGGGAAGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTACCATATACCTACG 289
QY 182 TAGACACTGTGAGGCGCGATTCCACCTCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
DB 290 CAGACTCTGTGAAGGCGGATTCCACCTCTCCAGAGACAAGCCCAAGCACTGTATC 349
QY 242 TGCAAACTCACTCTGAGAGCCGAGGACAGCGCTGTATTACTGTCCAGACATA 298
DB 350 TGCAAACTGAGAGCGCTGAGAGCCGAGGACAGCGCTGTATTACTGTCCGAGCCATA 406

RESULT 10
AW402895 412 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BKO-aaw-d-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3055170 5', mRNA sequence.
ACCESSION AW402895
VERSION AW402895.1 GI:6921669
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
1. 412
Location/Qualifiers
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p7773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 102 a 116 c 153 g 120 t

Query Match 61.8%; Score 217; DB 90; Length 491;
Best Local Similarity 78.7%; Pred. No. 2e-55;
Matches 259; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 2 AGGTCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 61
DB 128 AGGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 187
QY 62 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 121
DB 188 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 247
QY 122 CGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 181
DB 248 CAGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 307
QY 182 TAGACACTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 241
DB 308 CAGACTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 367
QY 242 TGCAGTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 301
DB 368 TGCAGTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 427
QY 302 ACAGGAGTGTGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 330
DB 428 ATAGCAGTGTGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 456

RESULT 15
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LOCUS UI-HF-BK0-aap-a-04-0-UI.r1 NIH_MGC_36 Homo sapiens CDNA clone
DEFINITION IMAGE:3054247 5', mRNA sequence.
ACCESSION AW402029 GI:6920715
VERSION EST.
KEYWORDS human.
SOURCE ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 518)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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/note="Vector: p7773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 99 a 149 c 148 g 121 t 1 others

Query Match 61.6%; Score 216.2; DB 90; Length 518;
Best Local Similarity 83.6%; Pred. No. 3.5e-55;
Matches 245; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 61
DB 54 ACGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 113
QY 62 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 121
DB 114 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 173
QY 122 CGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 181
DB 174 CAGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 233
QY 182 TAGACACTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 241
DB 234 CAGACTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 293
QY 242 TGCAGTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 294
DB 294 TGCAGTGTGAGAGTCTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCTGAGACTCT 346

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 08:23:45 ; Search time 103.87 seconds
(without alignments)
1269.448 Million cell updates/sec

Title: US-08-790-540A-1

Perfect score: 351

Sequence: 1 CAGGTCAGCTGCTGGAGTC.....CTACAGTCACTGTTCTAGT 351

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

- 1: /SID56/gcgdata/geneseq/geneseqn/NA1980.DAT:**
- 2: /SID56/gcgdata/geneseq/geneseqn/NA1981.DAT:**
- 3: /SID56/gcgdata/geneseq/geneseqn/NA1982.DAT:**
- 4: /SID56/gcgdata/geneseq/geneseqn/NA1983.DAT:**
- 5: /SID56/gcgdata/geneseq/geneseqn/NA1984.DAT:**
- 6: /SID56/gcgdata/geneseq/geneseqn/NA1985.DAT:**
- 7: /SID56/gcgdata/geneseq/geneseqn/NA1986.DAT:**
- 8: /SID56/gcgdata/geneseq/geneseqn/NA1987.DAT:**
- 9: /SID56/gcgdata/geneseq/geneseqn/NA1988.DAT:**
- 10: /SID56/gcgdata/geneseq/geneseqn/NA1989.DAT:**
- 11: /SID56/gcgdata/geneseq/geneseqn/NA1990.DAT:**
- 12: /SID56/gcgdata/geneseq/geneseqn/NA1991.DAT:**
- 13: /SID56/gcgdata/geneseq/geneseqn/NA1992.DAT:**
- 14: /SID56/gcgdata/geneseq/geneseqn/NA1993.DAT:**
- 15: /SID56/gcgdata/geneseq/geneseqn/NA1994.DAT:**
- 16: /SID56/gcgdata/geneseq/geneseqn/NA1995.DAT:**
- 17: /SID56/gcgdata/geneseq/geneseqn/NA1996.DAT:**
- 18: /SID56/gcgdata/geneseq/geneseqn/NA1997.DAT:**
- 19: /SID56/gcgdata/geneseq/geneseqn/NA1998.DAT:**
- 20: /SID56/gcgdata/geneseq/geneseqn/NA1999.DAT:**
- 21: /SID56/gcgdata/geneseq/geneseqn/NA2000.DAT:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	351	100.0	351	19 V49820	Vitaxin antibody h
2	302.2	86.1	351	19 V49822	LM609 antibody hea
3	268.6	76.5	482	11 Q05555	Sequence encoding
4	263.8	75.2	417	15 Q62804	Humanised murine K
5	263.8	75.2	417	16 Q87534	Humanised anti-KC-
6	259.6	74.0	582	18 T90020	DNA encoding heavy
7	259.6	74.0	761	20 X01214	Human antiFc epsil
8	259.6	74.0	770	20 X01216	Human antiFc epsil
9	257.4	73.3	413	15 Q68650	Mab A33 heavy cha
10	257.4	73.3	721	20 V99765	A33/212 single-cha
11	257.4	73.3	721	21 Z37397	Linked fusion prot
12	257.4	73.3	733	20 V99766	A33/218 single-cha

13	257.4	73.3	733	21	Z37398	Linked fusion prot
14	255	72.6	1938	19	V58929	A33 chimeric recep
15	252.4	71.9	411	19	V24243	Chimeric antibody
16	252.4	71.9	411	20	X00116	Human antibody hea
17	252.4	71.9	411	21	Z58914	DNA seq ID No: 58
18	251	71.5	351	16	Q96284	Human IgE receptor
19	249.4	71.1	351	16	T90025	Human IgE receptor
20	249.4	71.1	351	18	T90025	cDNA encoding heav
21	249.2	71.0	411	19	V24232	Chimeric antibody
22	249.2	71.0	411	20	X00092	Mouse humanised an
23	249.2	71.0	411	21	Z58913	Mouse antibody H c
24	247.4	70.5	369	19	V07642	anti-CD22 monoclon
25	246.8	70.3	1329	18	T61281	Humanised anti-L-s
26	246.2	70.1	480	13	Q20070	MRK16-H chain. Ch
27	244.8	69.7	418	15	Q62764	Murine KC-4 immuno
28	244.8	69.7	418	15	Q62789	Murine KC-4 immuno
29	244.4	69.6	722	21	Z28996	Anti-human CTLA-4
30	244.4	69.6	729	21	Z28997	Anti-murine CTLA-4
31	243.6	69.4	414	21	Z35243	Humanised anti-ver
32	242.2	69.0	324	13	Q20303	B cell hybridoma 1
33	241.4	68.8	357	15	Q66409	VH coding region o
34	240.6	68.5	360	19	V04636	Chimeric humanised
35	240.6	68.5	720	19	V04638	Chimeric humanised
36	240.2	68.4	354	18	T43417	Xenograft antibody
37	240	68.4	441	18	T72269	Chimeric MAB 15 FC
38	239.8	68.3	357	19	V44997	15D3 antibody heav
39	239.8	68.3	357	20	Z10957	15D3 VH chain codi
40	239.8	68.3	357	20	V08933	Antibody 15D3 heav
41	239	68.1	445	18	T72237	Humanised reshaped
42	238.4	67.9	457	18	T72267	Mouse Mab 15 heavy
43	238.2	67.9	445	14	Q36530	Chimeric MAB heavy
44	238.2	67.9	445	14	Q36537	BR55-2 heavy chain
45	238.2	67.9	491	14	Q36535	BR55-2 murine IgG3

ALIGNMENTS

RESULT 1

ID V49820 standard; DNA; 351 BP.

XX AC V49820;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region DNA.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT CDS 1..351

XX FT /*tag= a

XX FT /product= "vitaxin antibody heavy chain variable region"

XX FT /note= "partial sequence, no start or stop codon given"

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

```
XX WPI: 1998-437472/37.
DR P-PSDB; W76001.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 3; Fig 1a; 129pp; English.
XX
CC This sequence encodes the vitaxin antibody variable heavy chain region.
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match      100.08; Score 351; DB 19; Length 351;
Best Local Similarity 100.08; Pred. No. 5.9e-100; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 0;

QY 1 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGTGTGCAGCTTGGAGGTCCCTGAGACTC 60
DB 1 caggTgcagctggtagtctggggaggcggtgtgtgcagcttggaggtccctgagactc 60
QY 61 TCCGTGCGACCTCTGGATTACCTTCAGTACGTATGACATGCTTGGTTCGCCAGGCT 120
DB 61 tccgtgcagctctggattacccttcagtagctatgacatgtctgggttcgccaggct 120
QY 121 CCGGCGCAGGGTCTGGAGTGGTGCAGAAAGTACGTAGTGGTGGTGGTACCTACTAT 180
DB 121 cccggcgagggtctggagtggtgcgaaagttagtgggtgggtggtagcactactat 180
QY 181 TTAGACACTGTGAGGCGGATTCACCATCTCCAGAGCAATAGTAAGAACACCCCTATAC 240
DB 181 ttagacactgtgagggcgattaccattctccagagacaatagtaagaacacccctatac 240
QY 241 CTGCAAAATGAATCTCTGAGAGCCGAGGACACAGCCGCTATTACTGTGCAAGACATAAC 300
DB 241 ctgcaaatgaactctctgagagccgaggacacagccgtgtattactgtgcaagacataac 300
QY 301 TACGCGAGTTTGGCTTACTGGGCGCAAGGACTACAGTGACGTGTTCTAGT 351
DB 301 tacgcgagtttggcttactgggcgcaaggactacagtgacgtggttcttagt 351

RESULT 2
V49822
ID V49822 standard; DNA; 351 BP.
XX
XX AC V49822;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 antibody heavy chain variable region DNA fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; ss.
XX
OS Mus sp.
XX
```

```
Key Location/Qualifiers
CDS 1..351
FT /*tag= a
FT /product= "LM609 antibody heavy chain variable region"
FT /note= "partial sequence, no start or stop codon given"
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX Humanised antibody, vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 37; Fig 2a; 129pp; English.
XX
XX This sequence encodes the LM609 antibody variable heavy chain region.
XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX block integrin-mediated signal transduction. This is useful in the
XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match      86.18; Score 302.2; DB 19; Length 351;
Best Local Similarity 91.98; Pred. No. 8.7e-85;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTCTGGAGTCTGGGGAGGCGTGTGTGCAGCTTGGAGGTCCCTGAGACTCT 61
DB 2 aagTgcagctgtgagTctggggaggcttagTgaagcctggaggTccctgagactct 61
QY 62 CCTGTGCAGCTCTGGAGTTCACCTTCAGTACGTATGACATGCTTGGGTTCGCCAGGCTC 121
DB 62 cctgtgcagctctggagTtcaccttcagTtagtgcagctctgtgggttcgccagattc 121
QY 122 CGGCAAGGGTCTGGAGTGGTTCGCAAAAGTATAGTGGTGGTGGTAGCACCTACTATT 181
DB 122 cgggaagaggctggagTggTcgcaaaagtagtggTggTggtagcaccTactatt 181
QY 182 TAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGCAATAGTAAGAACACCCCTATACC 241
DB 182 tagacactgtgcagggcgattccacctctccagagacaatgccaagaacacccctatacc 241
QY 242 TGCAAAATGAATCTCTGAGAGCCGAGGACACAGCCGCTGTTACTGTGCAAGACATAACT 301
DB 242 tgcaaatgagcagTctgaactctgaggacacagccatgtattactgtgcaagacataact 301
QY 302 ACGCAGTTTGGCTTACTGGGCGCAAGGACTACAGTACGTGTTCT 348
DB 302 acgcagtttgcTtactgggccaaggactctggTcactgtctct 348

RESULT 3
Q05555
```

ID Q05555 standard; DNA; 482 BP.

XX AC Q05555;

XX DT 10-DEC-1990 (first entry)

XX DE Sequence encoding variable region of murine AHT 54 heavy chain.

XX KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX CDS 75..482

XX FT /*tag= a

XX PN EP380068-A.

XX PD 01-AUG-1990.

XX PF 24-JAN-1990; 90EP-0101351.

XX PR 04-DEC-1989; 89US-0441702.

XX PR 24-JAN-1989; 89US-0301216.

XX XX (MOLE-) MOLECULAR THERAPEU.

XX XX Zerler B;

XX XX WPI; 1990-232892/31.

XX XX P-PSDB; R06251.

XX PT Expression vectors for producing chimeric monoclonal antibodies -

XX PT which express human constant region and non-human variable region

XX PS Disclosure; ; P; English.

XX CC MABS comprising mouse CH and CL constant regions which human

XX CC variable regions may be used to create mouse/human hybrid MABS,

XX CC which have a longer serum half-life. Method can be used to produce

XX CC Abs against interleukin-2 receptor and tumour necrosis factor.

XX SQ Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;

Query Match 76.5%; Score 268.6; DB 11; Length 482;
Best Local Similarity 85.9%; Pred. No. 2.7e-74; Mismatches 0; Gaps 0;
Matches 298; Conservative 0; Indels 49; Gaps 0;

Oy 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGCTGTGTCAGCCTGGAGGTCCTCGAGACTCT 61

Db 133 aagtcagctgtgagctctggggagccttagtagaagcctggaggtccctgaactct 192

Oy 62 CCGTGTGAGCTCTGGATTCACCTTCAGTAGTATGACATGCTTGGTTCGCCAGGCTC 121

Db 193 cctgtgcagcctctggtattcgctttcagtagcattgacatgcttgggtgcccagactc 252

Oy 122 CGGGCAAGGCTCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTACGACCTACTATT 181

Db 253 cggagaagagctgtgagtggtggtcgatacattagtagtgggtggtgatacactactatc 312

Oy 182 TAGACATGTGCGAGGCGGATTCACCTCTCCAGAGCAATAGTAGAAGACACCCATATACC 241

Db 313 cagacactgtgaagggccgattccaccattctccagagacaatgccagacacccctttacc 372

Oy 242 TGCAATGAACCTCTCTGAGAGCCGAGGACAGACCGCTGTTACTGTGCAAGACATAACT 301

Db 373 tgcacaatgagcagctgtgaagctgtgagcacagcgctgtattactgtccaagaggtacg 432

Oy 302 ACGGCAAGTTTCTTACTTGGGGCCCAAGGACTACAGTACTGTTTCTT 348

Db 433 gctccctttgttacttggggcccaaggaactctgtgtcactgtctct 479

RESULT 4

O62804

XX Q62804 standard; DNA; 417 BP.

XX AC Q62804;

XX DT 25-JAN-1995 (first entry)

XX DE Humanised murine KC-4 immunoglobulin heavy chain V-region DNA.

XX KW Immunoglobulin variable domain; primer; polymerase chain reaction;

XX KW chimeric antibody; human mammary fat globule; human breast carcinoma;

XX KW murine anti-HMFG monoclonal antibody KC-4; humanised analogue; ss.

XX OS Chimeric Mus musculus.

XX OS Chimeric Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..416

XX FT /*tag= a

XX FT /note= "humanised KC-4 VH chain"

XX FT 58..416

XX FT /*tag= b

XX FT /product= heavy_chain_V-region

XX FT /note= "humanised framework region"

XX PN W09411509-A.

XX PD 26-MAY-1994.

XX PF 16-NOV-1993; 93WO-US11445.

XX PR 16-NOV-1992; 92US-0977696.

XX PR 30-SEP-1993; 93US-0129930.

XX PR 08-OCT-1993; 93US-0134346.

XX XX (CANC-) CANCER RES FUND CONTRA COSTA.

XX XX Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;

XX XX WPI; 1994-183510/22.

XX XX P-PSDB; R52823.

XX PT New analogue peptide(s) comprising antibody variable regions -

XX PT used to develop prods. for use in the detection, diagnosis,

XX PT therapy and prevention of neoplasms

XX PS Example 67; Page 91; 109pp; English.

XX CC This DNA sequence encodes a humanised murine anti-human carcinoma

XX CC antibody heavy chain variable region. The humanised antibody is

XX CC useful for carcinoma therapy and diagnosis and for in vivo imaging

XX CC of neoplastic cells. It is also of use in inhibiting the growth of

XX CC a primary or metastasised neoplasm.

XX SQ Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;

Query Match 75.2%; Score 263.8; DB 15; Length 417;
Best Local Similarity 85.8%; Pred. No. 8e-73;
Matches 308; Conservative 0; Mismatches 42; Indels 9; Gaps 1;

Oy 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGCTGTGTCAGCCTGGAGGTCCTCGAGACTCT 61

Db 59 aagtcagcatggtgagctctggggagccttagtagcagcctggaggggtccctgagactct 118

Oy 62 CCGTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121

Db 119 cctgtgcagcctctggattccttccagtagctatgccatgcttcttgggttcgaggtc 178

Oy 122 CGGGCAAGGCTCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTGGTACGACCTACTATT 181

Db 179 cagggaagggtggtggtgcagaaatagtagtgggtggttaattacgactactatc 238
QY 182 TAGACACTGTGAGGCGGCGATTCACCATCTCCAGACACATAGTAGACACACCCCTATACC 241
Db 239 aagacactgtgagcgccgcatccaccatctccagagacattcccaagaacacccctgtacc 298
QY 242 TCGAATGAACCTCTCTGAGAGCGGAGGACACACGCCGTGTATTACTGTGCAAGACATAACT 301
Db 299 tgcaaatgaacagtgtgaggtgagacacgcccgtgtattactgtgcaaggaggact 358
QY 302 ACGG-----CAGTTTGTCTACTGGGCGGAGGACTACAGTACTGTTTCTAGT 351
Db 359 acggtatcccgccgtgtgttactggtggcgaaggactctgtcactgtctctagt 417

RESULT 5
Q87534 standard; DNA; 417 BP.
XX
AC Q87534;
XX
DT 27-OCT-1995 (first entry)
XX
DE Humanised anti-KC-4 antibody VH FR-HZ.
XX
KW Anti-KC-4 antibody; humanised antibody; cancer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..417
FT /*tag= a
XX
PN WO9510776-A.
XX
PD 20-APR-1995.
XX
PF 16-NOV-1993; 93WO-US11444.
XX
PR 08-OCT-1993; 93US-0134346.
XX
PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
XX
PI Ceriani RL, Docouto JJR, Peterson JA;
XX
DR WPI: 1995-161912/21.
DR P-PSDB; R70471.
XX
PT New humanised anti-KC-4 monoclonal antibody - used for detection of
PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
PT cancers
XX
PS Claim 23; Table 22, Page 46; 61pp; English.
XX
CC Hybridomas were prepd. based on the anti-KC-4 mouse hybridoma AFCC
CC HB 8710 (US4708930). The murine variable regions were modified at
CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
CC humanised DNA sequences for the VH and VL segments are shown in
CC Q87534 and Q87533 respectively. Plasmid constructions comprising
CC the humanised variable regions and the human constant regions were
CC then used to transform SGP2/0-Ag14 myeloma cells to produce the
CC humanised anti-KC-4 MABs. The deduced AA sequences of the
CC humanised anti-KC-4 variable light and heavy chains are given in
CC R70470 and R70471 respectively.
XX
SQ Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;

Query Match 75.2%; Score 263.8; DB 16; Length 417;
Best Local Similarity 85.8%; Pred No. 86-73;
Matches 308; Conservative 0; Mismatches 42; Indels 9; Gaps 1;
QY .2 AGTGCAGCTGTGGAGTCTGGGGGAGCGGTTGTGCGCCTGGAGGTCCTCGAGACTCT 61

Db 59 aagtgcagatgtgagctgtggagggttagtgacgcctggagggtccctgagactct 118
QY 62 CCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCTTGGTTCCGCCAGGCTC 121
Db 119 cctgtgcagctctggattcgcctcttcagtagctagccattcttgggttcgcagggctc 178
QY 122 CGGCAAGGGTCTGAGTGGGTGCGAAAGTATTAGTGTGGTGGTAGCACCCTACTATT 181
Db 179 cagggaagggtgaggtggtgcagaaatagtagtgggtggttaattacgactactatc 238
QY 182 TAGACACTGTGAGGCGGCGATTCACCATCTCCAGACACATAGTAGACACACCCCTATACC 241
Db 239 aagacactgtgagcgccgattccaccatctccagagacattcccaagaacacccctgtacc 298
QY 242 TCGAATGAACCTCTCTGAGAGCGGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT 301
Db 299 tgcaaatgaacagtgtgaggtgagacacgcccgtgtattactgtgcaaggaggact 358
QY 302 ACGG-----CAGTTTGTCTACTGGGCGGAGGACTACAGTACTGTTTCTAGT 351
Db 359 acggtatcccgccgtgtgttactggtggcgaaggactctgtcactgtctctagt 417

RESULT 6
T90020
ID T90020 standard; DNA; 582 BP.
XX
AC T90020;
XX
DT 12-DEC-1997 (first entry)
XX
DE DNA encoding heavy chain variable region of human CRA2 antibody.
XX
KW Complementarity determining region; CDR: murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IGE; MAB; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2; ds.
XX
OS Homo sapiens.
XX
PN JP09191886-A.
XX
PD 29-JUL-1997.
XX
PF 19-JAN-1996; 36JP-0024816.
XX
PR 19-JAN-1996; 96JP-0024816.
XX
PA (ASAK) ASAHI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHIN KK.
PA (TSUR/) TSURA T.
XX
XX WPI: 1997-429186/40.
XX
DR Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IGE receptor - useful medicinally and have low
PT antigenicity in humans
XX
PS Disclosure: Fig 9; 26pp; Japanese.
XX
CC The present sequence, which encodes the heavy chain variable
CC region of the human antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAB), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAB. The humanised,
CC semi-chimeric or chimeric MAB can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
XX
SQ Sequence 582 BP; 133 A; 134 C; 155 G; 160 T; 0 other;

Query Match 74.0%; Score 259.6; DB 18; Length 582;
Best Local Similarity 84.4%; Pred. No. 1.8e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGGAGGCTGTGTCAGCCTGGAAGTCCCTGAGACTCT 61
DB 220 aggtgcagctgtggagctgtggggaggttggctcagcgtggggggtccctgagactct 279
QY 62 CCGTGCAGCCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCGAGGCTC 121
DB 280 cctgtgcagcctgtggatccaccttagtaccctatcccatgtcttgggtccgcaggtc 339
QY 122 CGGCAAGGCTGTGGAGTCTGGGGTGCAGAAAGTTAGTAGTGTGGTGTGACACTACTATT 181
DB 340 cagggaagggtggtggtggtccttccattagtagtaattggtggtgtagcaccctactc 399
QY 182 TAGACACTGTGAGGCGCCATTCACCATCTCCAGAGACAATAGTAGACACACCTATACC 241
DB 400 cagacactgtaaaggccggtattccacctctccagagacacgccaagaactcactgtatc 459
QY 242 TGCAGATGAACCTCTCGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
DB 460 tgcaaatgaacgcttgagagccgagacacacggtgtgtattactgtgcgagacataatt 519
QY 302 ACGGCAGTTTGTCTACTCGGCGCAAGGAGCTACACTGACTGTTTC 347
DB 520 atggagggaatggactactgggggcaaggaccacggtccaccgtctc 565

RESULT 7
X01214
ID X01214 standard; cDNA to mRNA; 761 BP.
XX
AC X01214;
XX
DT 31-MAR-1999 (first entry)
XX
DE Human antiFc epsilon RI alpha chain antibody coding sequence #2.
XX
KW AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..753
FT /*tag= a
FT sig_peptide 34..90
FT /*tag= b
FT mat_peptide 91..750
FT /*tag= c
XX
PN JP11000174-A.
XX
PD 06-JAN-1999.
XX
PF 13-JUN-1997; 97JP-0171232.
XX
PR 13-JUN-1997; 97JP-0171232.
XX
PA (ASAK) ASAHI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHI KK.
PA (TSUR/) TSURA T.
XX
DR WPI; 1999-124394/11.
DR P-PSDB; W73874.
XX
PT Preparing an antibody Fab fragment using yeast - in high yield
XX
PS Claim 6; Page 7; 13pp; Japanese.
XX
CC This sequence encodes a human antiFc epsilon RI alpha chain antibody;

CC produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast *Pichia pastoris* as the host cell. The method can prepare an antibody Fab fragment cost efficiently and in high yield.

QY 2 AGGTGACGCTGTGGAGTCTGGGGGAGGCTGTGTCAGCCTGGAAGTCCCTGAGACTCT 61
DB 92 aggtgcagctgtggagctgtggggaggttggctcagcgtggggggtccctgagactct 151
QY 62 CCGTGCAGCCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCGAGGCTC 121
DB 152 cctgtgcagcctgtggatccaccttagtaccctatcccatgtcttgggtccgcaggtc 211
QY 122 CGGCAAGGCTGTGGAGTCTGGGGTGCAGAAAGTTAGTAGTGTGGTGTGACACTACTATT 181
DB 212 cagggaagggtggtggtggtccttccattagtagtaattggtggtgtagcaccctactc 271
QY 182 TAGACACTGTGAGGCGCCATTCACCATCTCCAGAGACAATAGTAGACACACCTATACC 241
DB 272 cagacactgtaaaggccggtattccacctctccagagacacgccaagaactcactgtatc 331
QY 242 TGCAGATGAACCTCTCGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
DB 332 tgcaaatgaacgcttgagagccgagacacggtgtgtattactgtgcgagacataatt 391
QY 302 ACGGCAGTTTGTCTACTCGGCGCAAGGAGCTACACTGACTGTTTC 347
DB 392 atggagggaatggactactgggggcaaggaccacggtccaccgtctc 437

Query Match 74.0%; Score 259.6; DB 20; Length 761;
Best Local Similarity 84.4%; Pred. No. 2e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGGAGGCTGTGTCAGCCTGGAAGTCCCTGAGACTCT 61
DB 92 aggtgcagctgtggagctgtggggaggttggctcagcgtggggggtccctgagactct 151
QY 62 CCGTGCAGCCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCGAGGCTC 121
DB 152 cctgtgcagcctgtggatccaccttagtaccctatcccatgtcttgggtccgcaggtc 211
QY 122 CGGCAAGGCTGTGGAGTCTGGGGTGCAGAAAGTTAGTAGTGTGGTGTGACACTACTATT 181
DB 212 cagggaagggtggtggtggtccttccattagtagtaattggtggtgtagcaccctactc 271
QY 182 TAGACACTGTGAGGCGCCATTCACCATCTCCAGAGACAATAGTAGACACACCTATACC 241
DB 272 cagacactgtaaaggccggtattccacctctccagagacacgccaagaactcactgtatc 331
QY 242 TGCAGATGAACCTCTCGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
DB 332 tgcaaatgaacgcttgagagccgagacacggtgtgtattactgtgcgagacataatt 391
QY 302 ACGGCAGTTTGTCTACTCGGCGCAAGGAGCTACACTGACTGTTTC 347
DB 392 atggagggaatggactactgggggcaaggaccacggtccaccgtctc 437

RESULT 8
X01216
ID X01216 standard; cDNA to mRNA; 770 BP.
XX
AC X01216;
XX
DT 31-MAR-1999 (first entry)
XX
DE Human antiFc epsilon RI alpha chain antibody coding sequence #4.
XX
KW AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..762
FT /*tag= a
FT sig_peptide 34..99
FT /*tag= b
FT mat_peptide 100..759
FT /*tag= c
XX
PN JP11000174-A.
XX
PD 06-JAN-1999.
XX
PF 13-JUN-1997; 97JP-0171232.
XX
PR 13-JUN-1997; 97JP-0171232.
XX
PA (ASAK) ASAHI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHI KK.
PA (TSUR/) TSURA T.
XX
DR WPI; 1999-124394/11.

```
DR P-PSDB; W73876.
XX Preparing an antibody Fab fragment using yeast - in high yield
XX Claim 6; Page 9-10; 13pp; Japanese.
XX This sequence encodes a human antiFc epsilon RI alpha chain antibody,
CC produced using the method of the invention. The method is for preparing
CC an antibody Fab fragment using the yeast Pichia pastoris as the host
CC cell. The method can prepare an antibody Fab fragment cost efficiently
CC and in high yield.
XX Sequence 770 BP; 172 A; 223 C; 205 G; 170 T; 0 other;
SQ
Query Match 74.0%; Score 259.6; DB 20; Length 770;
Best Local Similarity 84.4%; Pred. No. 2e-71;
Matches 292; Conservative 0; Mismatches 54; Idels 0; Gaps 0;
QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGCAGCTGGAAGGTCCCTGAGACTCT 61
DB 101 aggtgcagctgtggaagtcgtgggagagcttggtccagcctgggggtccctgagactct 160
QY 62 CCGTGCAGCCTCTGATTCAGTTCAGTAGTATGACATGCTCTGGGTTCGCCAGGCTC 121
DB 161 cctgtgagcctctggtacccttttagtaccctaccctgctgtggtccgaggtc 220
QY 122 CGGCAAGGCTGTGGAGTGGTGCAGAAAGTTAGTAGTGTGTGTAGCACCTACTATT 181
DB 221 cagggaaggggtgagtggtgggtccttcattagtaagctggtgtgtagcactatc 280
QY 182 TAGACACTGTGAGGCGCCGATTCACCATCTCCAGAGACAAATAGTAAGAACACCTATAC 241
DB 281 cagacactgaaggccgattccaccatctccagagacacccaaagaactcactgtatc 340
QY 242 TGAATGAACTCTCTGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
DB 341 tgcataatgaacgcctgagagcggagacagcgctgtgtattactgtgagacataatt 400
QY 302 ACGGCAGTTTCTTACTGCGGCCAGGAGGACTACAGTGACTGTTTC 347
DB 401 atggaggaatgactactgtgggcaaggagaccacggtcaccgtctc 446
RESULT 9
Q68650 ID Q68650 standard; DNA; 413 BP.
XX AC Q68650;
XX DT 13-FEB-1995 (first entry)
XX DE MAB A33 heavy chain coding sequence.
XX KW Polymerase chain reaction; primer; amplify; PCR; variable region; light;
KW heavy; chains; VL; VH; humanised; antibody; vectors; expression; human;
KW secretion; A33; Fab'(gamma/delta/cys); pC16; ompA signal; C-kappa;
KW pSKompa; pMR055; CH1 domains; hinge; deltaCys; pMR022; pR0109;
KW antigen; diagnosis; treatment; colorectal cancer; metastases; ss.
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX FH Key Location/Qualifiers
FT primer_bind 1..32 /*tag= a
FT CDS 6..413 /*tag= b
FT sig_peptide 6..62 /*tag= c
FT mat_peptide 63..413 /*tag= d
FT primer_bind 396..413
```

```
FT XX P-PSDB; W73876.
PN XX Preparing an antibody Fab fragment using yeast - in high yield
XX XX Claim 6; Page 9-10; 13pp; Japanese.
PD XX This sequence encodes a human antiFc epsilon RI alpha chain antibody,
XX 10-DEC-1993; 93MO-GB02529.
XX 10-DEC-1992; 92GB-0025853.
PR 22-JUL-1993; 93GB-0015249.
XX (CLLT ) CELLTech LTD.
XX Adair JR, King DJ, Owens RJ;
XX WPI: 1994-217881/26.
XX P-PSDB; R56962.
PT Humanised antibodies raised against A33 antigen - are used for
PT diagnosis or treatment of colorectal tumours and metastases
PS Example 1; Fig 3(ii); 90pp; English.
XX The sequences given in Q68649-50 encode the light and heavy chain
CC variable regions (VH and VL) of the humanised anti-A33 antibody of
CC the invention. These fragments were produced by PCR using the primer
CC sequences given in Q68624-48. The amplified fragments were used in the
CC construction of vectors for the expression and secretion of the chimeric
CC humanised A33. The amplified products were cleaved with BstBI and SphI
CC fragments were cloned into the human kappa light chain acceptor vector,
CC pMR1.1, and the human heavy chain, IgG1, acceptor vector, pMR011
CC respectively, to give chimeric expression vector pR0108 for the light
CC chain and pR0107 for the heavy chain. Proteins which bind the A33
CC antigen can be used in the diagnosis or treatment of colorectal cancers
CC and metastases.
XX SQ Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;
Query Match 73.3%; Score 257.4; DB 15; Length 413;
Best Local Similarity 83.9%; Pred. No. 7.8e-71;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGCAGCTGGAAGGTCCCTGAGACTCT 61
DB 64 aagtgaagctgtgtggagtcctggggagagcttagtgaagcctggaggggtccctgaaactct 123
QY 62 CCGTGCAGCCTCTGATTCAGTTCAGTAGTATGACATGCTCTGGGTTCGCCAGGCTC 121
DB 124 cctgtgcagctctggattcgcttccagctacatgacatgcttctgtggttcgcagactc 183
QY 122 CGGCAAGGCTGTGGAGTGGTTCGCCAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181
DB 184 cggagaagagctgtgagtggtgtcgcaaccattagtagtgggtggttagttacacactactatt 243
QY 182 TAGACACTGTGAGGCGCCGATTCACCATCTCCAGAGACAAATAGTAAGAACACCTATACC 241
DB 244 tagacagtgtgaaggccgattccaccatctccagagacagtgccaggaacacctatacc 303
QY 242 TGAATGAACTCTCTGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
DB 304 tgcataatgaacgcctgagagcggagacagcgctgtgtattactgtgagacactcgg 363
QY 302 ACGGCAGTTTCTTACTGCGGCCAGGAGGACTACAGTGACTGTTTCT 348
DB 364 tagtcccggttgcctactgtgggcaaggagactcgtggtcaccgctctc 410
RESULT 10
V99765 ID V99765 standard; DNA; 721 BP.
XX
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Best Local Similarity 83.9%; Pred. No. 9.6e-71;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTGAGACTCT 61
DB 365 aagtgaagctgtgagctgtgggaggttagtgagcctgaggggtccctgaaactct 424
QY 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTGGCCAGGCTC 121
DB 425 cctgtgagcctctggttcgctttagtacctatgacatgtcttgggttgcgagactc 484
QY 122 CGGGCAAGGCTGTGAGTGGGTGGCAAAAGTTAGTAGTGTGTGTGAGCCTACTATT 181
DB 485 cggagaagagctgagtgagtgcccaaccattagtagtggttagttacacctatt 544
QY 182 TAGACACTGTGAGGCGCGATTCACCATCTCCAGACAAATAGTAGAACACCCCTATACC 241
DB 545 tagacagtgaaggccattccaccatctccagacagtgccagggaacacctatacc 604
QY 242 TGAATGAACTCTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGACATAACT 301
DB 605 tgcaaatgacagctcagtgctgagacacagcctgttattactgtgacagactacgg 664
QY 302 ACGGCAAGTTTGTCTACTGGGCGCAAGGAGCTACAGTGTGCTTCT 348
DB 665 tagtcccgcttgcctactgggccaaggagactctgtgctactgtctct 711

RESULT 12
V99766
ID V99766 standard; DNA; 733 BP.
XX AC V99766;
XX DT 23-MAR-1999 (first entry)
XX DE A33/218 single-chain Fv coding sequence.
XX KW Linker: fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
XX KW multichain protein; immunoglobulin; single chain antibody Fv; cancer;
XX KW aggregation; ds.
XX OS Synthetic.
XX FH Key
XX FT CDS
XX FT 1..711
XX FT /tag- a
XX FT /product- "A33/218 scFv"
XX FT /note- "the start codon is not indicated"
XX FT misc_feature 1..321
XX FT /tag- b
XX FT /note- "sequence coding for A33 V1 region"
XX FT misc_feature 322..375
XX FT /tag- c
XX FT /note- "sequence coding for peptide linker 218"
XX FT misc_feature 376..708
XX FT /tag- d
XX FT /note- "sequence coding for A33 Vh region"
XX PN US5856456-A.
XX PD 05-JAN-1999.
XX PE 07-APR-1994; 94US-0224591.
XX PR 07-APR-1994; 94US-0224591.
XX PR 20-NOV-1992; 92US-0980529.
XX PR 15-JAN-1993; 93US-0002845.
XX PA (ENZO-) ENZON INC.
XX PI Filpula DR, Whitlow MD;
XX PN US5990275-A.
XX XX
```

WPI; 1999-105193/09.
P-PSDB; W95441.
DNA encoding fusion polypeptide including protease resistant linker
- for making single-chain Fv antibody fragments, e.g for diagnosis
and treatment of cancer
Disclosure; Fig.13; 39pp; English.
The invention is directed to a novel peptide linker useful for connecting
polypeptide constituents into a novel linked fusion polypeptide. The
peptide linker includes at least one XP motif (where X is a charged
amino acid) and includes any of these sequences (GTSGGSPGSGSGSGTKG;
GTSGSPGSGSGTKG; or GTSKSGSGK) to inhibit its proteolysis by
subtilisin or trypsin. DNA molecules encoding fusion polypeptides
containing two polypeptides, derived from the same multichain protein of
the immunoglobulin (Ig) superfamily and a peptide linker as above, are
particularly useful to prepare single chain antibody Fv fragments (scFv),
potentially useful for diagnosis and treatment of cancer. The fusion
polypeptide containing the specified linkers is proteolytically stable
(associated with positioning of the P residue) and resistant to
aggregation, while residue X improves solubility. The present sequence
represents the nucleotide sequence of a A33/218 scFv fragment.
Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 73.3%; Score 257.4; DB 20; Length 733;
Best Local Similarity 83.9%; Pred. No. 9.6e-71;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTGAGACTCT 61
DB 377 aagtgaagctgtgagctgtgggaggttagtgagcctgaggggtccctgaaactct 436
QY 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTGGCCAGGCTC 121
DB 437 cctgtgagcctctggttcgctttagtacctatgacatgtcttgggttgcgagactc 496
QY 122 CGGGCAAGGCTGTGAGTGGGTGGCAAAAGTTAGTAGTGTGTGCTGCTTCTACTATT 181
DB 497 cggagaagagctgagtgaggcgaacattagtagtgggttgcgagactctatt 556
QY 182 TAGACACTGTGAGGCGCGATTCACCATCTCCAGACAAATAGTAGAACACCCCTATACC 241
DB 557 tagacagtgaaggccattccaccatctccagagacagtgccagggaacacctatacc 616
QY 242 TGAATGAACTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB 617 tgcaaatgacagctcagtgctgagacacagcctgttattactgtgacagactacgg 676
QY 302 ACGGCAAGTTTGTCTACTGGGCGCAAGGAGCTACAGTGTGCTTCT 348
DB 677 tagtcccgcttgcctactgggccaaggagactctgtgctactgtctct 723

RESULT 13
237398
ID 237398 standard; DNA; 733 BP.
XX AC 237398;
XX DT 08-FEB-2000 (first entry)
XX DE Linked fusion protein A33/218 scFv coding sequence.
XX KW Fusion protein; linker; linked fusion polypeptide; multichain protein;
XX KW protein complex; antibody; ss.
XX OS Synthetic.
XX PN US5990275-A.
XX XX

PD 23-NOV-1999.

XX
XX 10-SEP-1997; 97US-0926789.
XX
XX 07-APR-1994; 94US-0224591.
PR 20-NOV-1992; 92US-0980529.
PR 15-JAN-1993; 93US-0002845.
XX
XX (ENZO-) ENZON INC.
XX
XX Filpula DR, Whitlow MD;
XX
XX WPI; 2000-022812/02.
DR P-PSDB; Y54837.
XX

PT Peptide linkers, linked fusion polypeptides containing the linkers and
PT their preparation -
XX
XX Example; Fig 13; 42pp; English.
XX

CC This sequence encodes a linked fusion protein containing the
CC amino acid linker of the invention. The linkers are used for connecting
CC constituent polypeptides to form novel linked fusion polypeptides.
CC Polypeptides derived from any protein can be connected, in particular
CC multichain protein or protein complexes e.g. enzymes, members of the
CC immunoglobulin superfamily, hormones, DNA-binding proteins. The linker
CC provides fusion proteins which have greater stability and are less
CC susceptible to aggregation.
XX

XX Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 73.3%; Score 257.4; DB 21; Length 733;
Best Local Similarity 83.9%; Pred. No. 9.6e-71;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGGTGAGTCACTTCGCGGAGCGGTGTGCAGCCTGGAAGTCTCTGAGACTCT 61
Db 377 aagtgaaagtgtggaagtctggaggagccttagtgaagccctggaggggtccccgaactct 436
QY 62 CCGTGCAGCCTCTGGATTCACTTCAGTACATGATGATGTTGGGTTGCCAGGCTC 121
Db 437 cctgtgcagcctctggattcgcttcagtaacctatgatgtctctgtgggttcgcagactc 496
QY 122 CGGCGAAGGCTCTGGAGTGGGTCCCAAAGTTAGTAGTGGTGGTAGCACTTACTATT 181
Db 497 cgagaagaagcgtggaatgggtgcgaaccattagtagtggtagttacactactatt 556
QY 182 TAGACACTGTGCAGGCGCGAATCACATCTCCAGAGACAATAGTAAGAACCCTATACC 241
Db 557 tagcaagtgtgaagggccgattcacctaccatctccagagacagtgccaggaacacctatacc 616
QY 242 TGCAATGAACTCTCAGAGCCGAGACACAGCCGCTGTATTACTGTGCAAGACATACT 301
Db 617 tgc aaatgagcagtctgaggtctgaggacacggcctgtattactgtgcaccgactacgg 676
QY 302 ACCGCGAGTTTGTCTACTGGGCGCAAGGACTACAGTGCATGTTTCT 348
Db 677 tagtcccgttgttactctggggccaaggactctggtcatctgtctct 723

RESULT 14
V58929 standard; DNA; 1938 BP.

ID V58929 standard; DNA; 1938 BP.
XX AC V58929;
XX AC
XX DT
XX DE
XX DE
XX DE
XX DE
XX DE
KW Chimeric receptor; A33; colorectal cancer; antigen; tumour;
KW cytotoxicity; gene therapy; signal transduction; monoclonal antibody;

KW		mouse; ss.
XX		
OS		Chimeric - Mus sp.
OS		Chimeric - Homc sapiens.
XX		
FH	Key	Location/Qualifiers
FT	CDS	7..1938
FT		/*tag= a
FT		
PX		WO9841613-A1.
PN		
XX		
DD		24-SEP-1998.
XX		
PF		13-MAR-1998; 98WO-US03797.
XX		
PR		14-MAR-1997; 97US-0815030.
XX		
PA	(CASE/)	CASENTINI-BOROCZ D.
PA	(FINE/)	FINER M H.
PA	(GREE/)	GREENBURG G B.
PA	(OTTE/)	OTTEN G R.
XX		
PI	Casentini-Borocz D,	Finer MH, Greenburg GB, Otten GR;
XX		
DR	WPI;	1998-521211/44.
DR	P-PSDB;	W73048.
XX		
PT	New chimeric DNA encoding membrane-bound receptor for non-MHC	
PT	restricted signal activation - inducing cytotoxic effector cells or	
PT	cytokine production in presence of tumour cells expressing the A33	
PT	antigen, and related vectors	
XX		
PS	Example 3;	Page: 42-43; 90pp; English.
XX		
CC	This DNA sequence codes for murine A33 chimeric receptor (see	
CC	W73048) comprising a signal peptide from the V kappa chain of human	
CC	antibody 98-6, light chain and heavy chain variable regions of	
CC	anti-colon cancer antigen A33 murine monoclonal antibody A33, human	
CC	IgG2 constant domain and M1 segment, human CD4 transmembrane domain	
CC	and an intracellular portion of human TCR-associated zeta chain. A	
CC	humanised version of the A33 chimeric receptor has been constructed	
CC	(see W73049). Novel chimeric proteins, and DNA encoding them, are	
CC	provided, in which the chimeric proteins are characterised by an	
CC	extracellular domain capable of binding to A33 in a non-MHC	
CC	restricted manner, a transmembrane domain and a cytoplasmic domain	
CC	capable of activating a signalling pathway. Binding of A33 to the	
CC	extracellular domain results in transduction of a signal and	
CC	activation of a signalling pathway in the cell, such that the cell	
CC	may be induced to carry out various functions relating to the	
CC	signalling pathway. The chimeric DNA may be used to modify	
CC	lymphocytes as well as haematopoietic stem cells as precursors	
CC	to a number of important cell types. The modified cells can be	
CC	transplanted (especially as a bone marrow transplant) into a mammal	
CC	to provide a source of cytotoxic effector cells that can kill cells	
CC	expressing the tumour-associated A33 antigen and cytokine producing	
CC	cells. The modified cells are activated in presence of A33+ cells.	
CC	Expression constructs and retrovirus vectors are provided.	
XX		
SQ	Sequence 1938 BP;	464 A; 543 C; 557 G; 374 T; 0 other;
XX		

	Query Match	72.6%	Score 255;	DB 19;	Length 1938;
	Best Local Similarity	84.0%;	Pred. No. 7.6e-70;		
	Matches 288;	Conservative 0;	Mismatches 55;	Indels 0;	Gaps
QY	2	AGGTGACGCTGTGTGAGTCTGGGGAGGCGTTGTGCAAGCTGGAAGTCCCTGAGACTCT	61		
Db	449	agatgaagcttctggagctctggggaggcttagtgaagcctggaggctccctgaaactct	50		
QY	62	CTGTGACGCTCTGGATTACCTTCACCTAGCTATGACATGTCTTGGGTGCGCAGGCTC	12		
Db	509	ctgtgacgacctgtgattcgtctcagtaactgacatgctcttggttgcgcgaactc	56		

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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 05:03:45 ; Search time 75.17 Seconds
(without alignments)
752.524 Million cell updates/sec

Title: US-08-790-540A-1
Perfect score: 351
Sequence: 1 CAGGTGACGTGTGTGAGTC.....CTACAGTACTGTTTCTAGT 351
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues
Total number of hits satisfying chosen parameters: 561672
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/PCRTUS_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.4	73.3	413	1	US-08-253-877C-56
2	257.4	73.3	413	2	US-08-452-164A-56
3	257.4	73.3	721	2	US-08-224-591-15
4	257.4	73.3	721	2	US-08-926-789-15
5	257.4	73.3	733	2	US-08-224-591-17
6	257.4	73.3	733	2	US-08-926-789-17
7	246.8	70.3	1329	4	PCT-US96-13152-3
8	244.8	69.7	418	1	US-07-977-696C-27
9	244.8	69.7	418	1	US-08-129-930B-27
10	240.6	68.5	360	2	US-08-672-176A-3
11	240.6	68.5	720	2	US-08-672-176A-5
12	239.8	68.3	357	1	US-08-475-000-15
13	239.8	68.3	357	2	US-08-483-199-15
14	239.8	68.3	357	2	US-08-484-508-15
15	238.2	67.9	445	1	US-08-053-171-10
16	238.2	67.9	491	1	US-08-053-171-6
17	237.2	67.6	717	2	US-08-553-497A-17
18	236.6	67.4	717	2	US-07-956-399-3
19	235.6	67.1	357	1	US-08-331-398A-21
20	235.6	67.1	357	1	US-08-207-996-26
21	235.6	67.1	357	2	US-08-760-840A-26
22	235.6	67.1	357	2	US-08-760-840A-27
23	235.6	67.1	357	2	US-08-331-397B-21
24	235.6	67.1	357	2	US-08-759-804A-21
25	235.6	67.1	357	3	US-09-266-119-26
26	235.6	67.1	357	3	US-09-266-119-27
27	235.6	67.1	375	1	US-08-331-398A-59
28	235.6	67.1	375	2	US-08-331-397B-59

29	235.6	67.1	375	2	US-08-759-804A-58
30	235.6	67.1	738	1	US-08-331-398A-31
31	235.6	67.1	738	2	US-08-331-397B-31
32	235.6	67.1	738	2	US-08-759-804A-31
33	235.4	67.1	923	4	PCT-US94-07659-1
34	234.8	66.9	417	1	US-08-398-613A-21
35	234.8	66.9	417	1	US-08-398-612A-21
36	234.8	66.9	417	1	US-08-398-611A-21
37	234.8	66.9	417	1	US-08-396-851A-21
38	234.8	66.9	417	2	US-08-491-334A-21
39	234.8	66.9	417	3	US-09-027-449-18
40	234.8	66.9	417	3	US-08-804-444A-18
41	234.8	66.9	417	3	US-09-026-985-18
42	234.8	66.9	756	1	US-08-398-613A-29
43	234.8	66.9	756	1	US-08-398-612A-29
44	234.8	66.9	756	1	US-08-398-611A-29
45	234.8	66.9	756	1	US-08-396-851A-29

ALIGNMENTS

RESULT 1
US-08-253-877C-56
; Sequence 56, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tscu, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne New Jersey
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253.877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: "nucleic acid"
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..413
US-08-253-877C-56

Query Match 73.3%; Score 257.4; DB 1; Length 413;
Best Local Similarity 83.9%; Pred. No. 3.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 61
DB 64 AAGTGAAGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAAACTCT 123
QY 62 CCGTGTGACGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 121
DB 124 CCGTGTGACGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 183
QY 122 CGGCAAGGGTCTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 181
DB 184 CGGCAAGGGTCTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 243
QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACATAGTAGAGACCCCTATACC 241
DB 244 TAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACATAGTAGAGACCCCTATACC 303
QY 242 TCGAATGAACCTCTGTGAGAGCGGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT 301
DB 304 TCGAATGAGCAGTCTGAGGCTGTGAGGACACGCGCTGTATTACTGTGCAAGCAGTACGG 363
QY 302 ACGGCAGTTTCTTACTGGGGCCCAAGGAGCTACAGTCACTGTTTCT 348
DB 364 TAGTCCCGTTTCTTACTGGGGCCCAAGGAGCTCTGTCACCGTCTCT 410

RESULT 2
US-08-452-164A-56
; Sequence 56, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452.164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 6..413
US-08-452-164A-56

Query Match 73.3%; Score 257.4; DB 2; Length 413;
Best Local Similarity 83.9%; Pred. No. 3.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 61
DB 64 AAGTGAAGCTGTGGAGTCTGGGGAGGGGTTGTGAAAGCTGGAGGGTCCCTGAAACTCT 123
QY 62 CCGTGTGACGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 121
DB 124 CCGTGTGACGCTGTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 183
QY 122 CGGCAAGGGTCTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 181
DB 184 CGGCAAGGGTCTGGAGTCTGGGGAGGGGTTGTGACGCTGGAAGGTCCCTGAGACTCT 243
QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACATAGTAGAGACCCCTATACC 241
DB 244 TAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACATAGTAGAGACCCCTATACC 303
QY 242 TCGAATGAACCTCTGTGAGAGCGGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT 301
DB 304 TCGAATGAGCAGTCTGAGGCTGTGAGGACACGCGCTGTATTACTGTGCAAGCAGTACGG 363
QY 302 ACGGCAGTTTCTTACTGGGGCCCAAGGAGCTACAGTCACTGTTTCT 348
DB 364 TAGTCCCGTTTCTTACTGGGGCCCAAGGAGCTCTGTCACCGTCTCT 410

RESULT 3
US-08-224-591-15
; Sequence 15, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224.591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540


```

; INFORMATION FOR SEQ ID NO: 15:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 721 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: both
;     TOPOLOGY: both
;
; FEATURE:
;     NAME/KEY: CDS
;     LOCATION: join(1..711)
; US-08-224-591-15

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Query Match	73.3%	Score	257.4	DB	2	Length	721
Best Local Similarity	83.9%	Pred.	No. 4.2e-77				
Matches	291	Conservative	0	Mismatches	56	Indels	0
							Gaps
QY	2	AGGTGCAGCTGGTGAGCTCGGGGAGGCGTTGTGCAGCCTGGAGGTCCCTGCAGACTCT	61				
DB	365	AGTGAACGCTGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT	424				
QY	62	CTGTGCAGCCTCTGGATTACACCTTCAGTAGCTATGACATGCTCTGGGTTGCCAGGCTC	121				
DB	425	CTGTGCAGCCTCTGGATTGCTTTTCAGTACCTATGACATGCTCTGGGTTGCCAGACTC	484				
QY	122	CGGCAAGGGTCTGGAGTGGGTGCGAAAGTTAGTGTGGTGGTAGCACCCTACTATT	181				
DB	485	CGGAGAGAGGCTGGAGTGGGTGCGAACCACTTAGTAGTGGTGGTAGTACACTACTATT	544				
QY	182	TAGACACTGTGCAGGGCGGATTCCACCATCTCCAGAGACAATAGTAAGNACACCCTATACC	241				
DB	545	TAGACAGTGTGAAGGGCGGATTCCACCATCTCCAGAGACAGTGCCAGGAAACACCCTATACC	604				
QY	242	TGCAAAATGAACCTCTCTCAGAGCCGAGACACAGCCGTGTATTACTGTGTCAAGACATAACT	301				
DB	605	TGCAAAATGACAGCTCTCAGGTCTCAGGACACAGGCGCTGTATTACTGTGCACCGCTACGG	664				
QY	302	ACGCGACTTTTGCTTACTTGGGGCCAAAGGACTACAGTGCAGTGTTCCT	348				
DB	665	TAGTCCCGTTTGCTTACTTGGGGCCAAAGGACTCTGGTCACTGTCTCT	711				

```

4
RESULT
US-08-926-789-15
; Sequence 15, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filipula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529

```

```

; FILING DATE: 20-NOV-1992
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Goldstein, Jorge A.
;
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCCT NUMBER: 0977.1920002/JAG
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
;
; INFORMATION FOR SEQ ID NO: 15:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: join(1..711)
;
; US-08-926-789-15

```

Query Match	73.3%;	Score	257.4;	DB 2;	Length	721;			
Best Local Similarity	83.9%;	Pred.	No. 4.2e-77;						
Matches	291;	Conservative	0;	Mismatches	56;	Indels	0;	Gaps	
QY	2	AGTGCAGCTGTGGAGTCTGGGGGAGGCGTTGTGCAGACCTGGAAGTCCCTGGAGACTCT	61						
DB	365	AGTGAAGCTTTGGAGTCTGGGGGAGGCTTGTGAAGCGCTGGAGGTCCCTGAAACTCT	424						
QY	62	CTGTGTGACGCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGGTTCCGACGGCTC	121						
DB	425	CTGTGTGACGCTCTGGATTCCGCTTCCTCAGTACCTATGACATGTCTTGGGTTGCCAGACTC	484						
QY	122	CGGGCAAGGGTCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTGTGACACCTACTATT	181						
DB	485	CGGAGAAGAGCGCTGGAGTGGGTGCGCAACATTAGTAGTGGTGGTATTACACTACTATT	544						
QY	182	TAGACACTGTGCAGGGCCGATTACCATCTCCAGAGACAATAGTAAAGACACCCCTATACC	241						
DB	545	TAGACAGTGTGAAGGGCCGATTACCATCTCCAGAGACAGTGGCAGGACACCCCTATACC	604						
QY	242	TGCAAAATGAACCTCTTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT	301						
DB	605	TGCAAAATGACAGCTCTGAGGCTTGAGGACACAGCCCTGTATTACTGTGACCAGCTACGG	664						
QY	302	ACGGCAGTTTTGCTTACTGGGGCCAAAGGACCTACAGTGCCTTTCT	348						
DB	665	TAGTCCCGTTTGGTTACTGGGGCCAAAGGACCTCTGGTCACTGTCTCT	711						

RESULT 5
US-08-224-591-17
; Sequence 17, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 500
; City: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224.591
; FILING DATE: Herewith

CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723)
US-08-224-591-17

Query Match 73.3%; Score 257.4; DB 2; Length 733;
Best Local Similarity 83.9%; Pred. No. 4.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 61
DB 377 AAGTGAAGCTTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 436
QY 62 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 121
DB 437 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 496
QY 122 CGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 181
DB 497 CGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 556
QY 182 TAGACACTGTGACAGGCGCGATTCCACCATCTCCAGAGACAATAGTAAGAACCCCTATACC 241
DB 557 TAGACAGTGTGAAGGCGCGATTCCACCATCTCCAGAGAGAGTCCAGGAACCCCTATACC 616
QY 242 TCAATGAAGTCTGTGAGAGCGGAGGACACAGCGCTGTATTACTGTGCAAGACATACT 301
DB 617 TCAATGAAGTCTGTGAGAGCGGAGGACACAGCGCTGTATTACTGTGCAAGACATACT 676
QY 302 ACGGCAAGTCTGTGAGAGCGGAGGACACAGCGCTGTATTACTGTGCAAGACATACT 348
DB 677 TAGTCCCGTTGCTTACTGGGCGCAAGGAGCTCTGGTCACTGCTCT 723

RESULT 6
US-08-926-789-17

Sequence 17, Application US/08926789
Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224,591
FILING DATE:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723)
US-08-926-789-17

Query Match 73.3%; Score 257.4; DB 2; Length 733;
Best Local Similarity 83.9%; Pred. No. 4.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 61
DB 377 AAGTGAAGCTTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 436
QY 62 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 121
DB 437 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 496
QY 122 CGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 181
DB 497 CGGCAAGGCTGTGGAGTCTGGGGAGGCGTTGTCCAGCCTGGAAGTCCCTGAGACTCT 556
QY 182 TAGACACTGTGACAGGCGCGATTCCACCATCTCCAGAGACAATAGTAAGAACCCCTATACC 241
DB 557 TAGACAGTGTGAAGGCGCGATTCCACCATCTCCAGAGAGAGTCCAGGAACCCCTATACC 616
QY 242 TCAATGAAGTCTGTGAGAGCGGAGGACACAGCGCTGTATTACTGTGCAAGACATACT 301
DB 617 TCAATGAAGTCTGTGAGAGCGGAGGACACAGCGCTGTATTACTGTGCAAGACATACT 676
QY 302 ACGGCAAGTCTGTGAGAGCGGAGGACACAGCGCTGTATTACTGTGCAAGACATACT 348
DB 677 TAGTCCCGTTGCTTACTGGGCGCAAGGAGCTCTGGTCACTGCTCT 723

RESULT 7
PCT-US96-13152-3
Sequence 3, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1,1329
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1
PCT-US96-13152-3

Query Match 70.3%; Score 246.8; DB 4; Length 1329;
Best Local Similarity 84.1%; Pred. No. 2e-73;
Matches 291; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 2 AGTGTGAGCTGGTGGAGTCTGGGGAGGCGTGTGTGAGCTGGAAGGTCCTGAGACTCT 61
DB 2 AAGTGCACTGGTGGAGTCTGGGGAGGCTTAGTGAGCTGGAGGAGCTTGGAGACTCT 61
QY 62 CTGTGACGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 121
DB 62 CTGTGACGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 121
QY 122 CGGCAAGGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 181
DB 122 CAGGGAAGGCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 178
QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGCAATAGTAGTGTGAGTGTGAGTGT 241
DB 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGCAATAGTAGTGTGAGTGTGAGTGT 241
QY 242 TGAACATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATACT 301
DB 242 TGAACATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATACT 301
QY 302 ACGGAGTTTGTACTGGGCGCAAGGAGCTACAGTGTGCTTTC 347
DB 299 ACGGAGTTTGTACTGGGCGCAAGGAGCTACAGTGTGCTTTC 344

RESULT 9

US-08-129-930B-27
; Sequence 27, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-129-930B-27

Query Match 69.7%; Score 244.8; DB 1; Length 418;
Best Local Similarity 82.9%; Pred No. 5,5e-73;
Matches 295; Conservative 0; Mismatches 52; Indels 9; Gaps 1;
QY 2 AGGTGACGTGGTGGAGTCTGGGGGAGCGGTTGTGCAGCCTGGAAGGTCCTCGAGACTCT 61
Db 59 AAGTCAGATGTGGAGTCTGGGGGAGCGGTTAGTGAAGCCTGGAGGTCCTCGAAACTCT 118
QY 62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121
Db 119 CTTGTGCAGCCTCTGGATTCAGTTCGCTATGATGCTATGCTTGGGTCGCCAGTCTC 178
QY 122 CGGGCAAGGGTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGTAGCAGCTACTATT 181
Db 179 CAGAGAGAGGCTGGAGTGGGTCGCGAATAGTAGTGGTGGTAAATAGCGCTACTATC 238
QY 182 TAGACACTGTGCAGGCGCGATTCACCTATCTCCAGAGACATAGTAAGACACCCCTATACC 241
Db 239 AAGACACTGTGAGCGGCGGATTCACCTATCTCCAGAGACATAGTAAGACACCCCTATACC 298
QY 242 TCCAATGACTCTCTGAGAGCGGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT 301
Db 299 TGGAAATGACGAGTCTGAGGTCGTGAGGACACGCGCCATGTATTACTGTGCAAGGGAGGACT 358

QY 302 ACGG-----CAGTTTCTCTACTGGGCCCAAGGAGCTACAGTACTGTTTCT 348
Db 359 ACGGTATCCCGCGCTGGTTGCTTACTGGGCCCAAGGAGCTCTGTTCTCTCTCT 414

RESULT 10

US-08-672-176A-3
; Sequence 3, Application US/08672176A
; Patent No. 5908925
; GENERAL INFORMATION:
; APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
; TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
; TITLE OF INVENTION: Specificity for Glycated Albumin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Exocell, Inc.
; STREET: 3508 Market Street, suite 420
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS 4.0 or better
; SOFTWARE: Wordperfect, Version 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,176A
; FILING DATE: unknown
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Robert S.
; REGISTRATION NUMBER: unknown
; REFERENCE/DOCKET NUMBER: E1042/20002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2010
; TELEFAX: 215-751-1142
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs/120 amino acid residues
; TYPE: nucleic acid/amino acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: humanized A717 heavy chain variable region
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE: synthetic
; ORGANISM: N/A
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELL: N/A
; IMMEDIATE SOURCE: plasmid
; LIBRARY: N/A
; CLONE: PHUA717VH-1
; POSITION IN GENOME: N/A
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE: human framework regions; murine CDRs
; NAME/KEY: FR-1; CDR-1; FR-2; CDR-2; FR-3; CDR-3; FR-4
; LOCATION: aa#31-35; aa#36-49; aa#50-66;
; LOCATION: aa#67-98; aa#99-109; aa#110-120

IDENTIFICATION METHOD: similarity to known sequences
OTHER INFORMATION: antigen is human glycosylated albumin
PUBLICATION INFORMATION: N/A

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO: 3:

US-08-672-176A-3

Query Match 68.5%; Score 240.6; DB 2; Length 360;
Best Local Similarity 82.3%; Pred. No. 1.3e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTGGAAGGTCCTGAGACTCT 61
DB 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTGGAAGGTCCTGAGACTCT 61
QY 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121
DB 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121
QY 122 CGGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
DB 122 CCGGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
QY 182 TAGACACTGTGAGGCGGCTTACCATCTCCAGAGACAATAGTAGAAGACACCTATACC 241
DB 182 TAGACACTGTGAGGCGGCTTACCATCTCCAGAGACAATAGTAGAAGACACCTATACC 241
QY 242 TCGAAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGA----- 294
DB 242 TCGAAATGAACTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGAGATGTT 301
QY 295 --CATAACTACGCGAGTTTGTCTTACTGGGCGGAGGAGGACTACAGTACTGTTTC 347
DB 302 ATCTTTTACTATGCTATGAGTACTGAGGCTTACGAGGCTCAAGGACACAGTCAACCGTCTC 356

RESULT 11

US-08-672-176A-5
Sequence 5, Application US/08672176A
Patent No. 5908925

GENERAL INFORMATION:

APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
TITLE OF INVENTION: Specificity for Glycosylated Albumin
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Exocell, Inc.
STREET: 3508 Market Street, suite 420
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104

COMPUTER READABLE FORM:

MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: PC
OPERATING SYSTEM: DOS 4.0 or better
SOFTWARE: Wordperfect, Version 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,176A
FILING DATE: unknown
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A

FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Silver, Robert S.
REGISTRATION NUMBER: unknown
REFERENCE/DOCKET NUMBER: E1042/20002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2010
TELEFAX: 215-751-1142
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs/240 amino acid residues
TYPE: nucleic acid/amino acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: humanized A717 immunoglobulin single-chain Fv
HYPOTHETICAL: yes
ANTI-SENSE: no
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE: synthetic
ORGANISM: N/A
STRAIN: N/A
INDIVIDUAL ISOLATE: N/A
DEVELOPMENTAL STAGE: N/A
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: plasmid
LIBRARY: N/A
CLONE: pHuA717ScFv-1
POSITION IN GENOME: N/A
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE: HuA717VH-1 linked to HuA717VL
NAME/KEY: HuA717VH; linker; HuA717VL
LOCATION: aa# 1-120; aa# 121-133; aa# 134-240
IDENTIFICATION METHOD: similarity to known sequences
OTHER INFORMATION: antigen is human glycosylated albumin
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5:
US-08-672-176A-5

Query Match 68.5%; Score 240.6; DB 2; Length 720;
Best Local Similarity 82.3%; Pred. No. 1.3e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTGGAAGGTCCTGAGACTCT 61
DB 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTGGAAGGTCCTGAGACTCT 61
QY 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121
DB 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121
QY 122 CGGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
DB 122 CCGGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
QY 182 TAGACACTGTGAGGCGGCTTACCATCTCCAGAGACAATAGTAGAAGACACCTATACC 241

Db	182	CAGACAGTGTGAAGGGCCGATTCCACATCTCCAGAGACAATTCGAGAACACAGCTTGACC	241
QY	242	TGCAAAATGAATCTCTCAGAGCCGAGGACACAGCCGTGTTACTGTGCAAGA-----	294
Db	242	TGCAAAATGACAGTCTCAGGGCTGTGAGGACACAGCCGTGTTACTGTGCAGAGAGATGGTT	301
QY	295	--CATAACTACGGCAGTGTTCCTTACTGGGGCCAAAGGACTACAGTGACTGTTC	347
Db	302	ATCTTTTATTACTATGCTATGGACTACTGGGGTCAAGGAACACAGTCAACCGTCTC	356

RESULT 12
 US-08-475-000-15
 Sequence 15, Application US/08475000
 Patent No. 5811267
 GENERAL INFORMATION:
 APPLICANT: RING, DAVID B.
 TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON CORPORATION
 STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94662-8097
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/475,000
 APPLICATION NUMBER: US/08/475,000
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: SAVEREIDE, PAUL
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0850.007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2585
 TELEFAX: (510) 655-3542
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..357
 US-08-475-000-15

Query Match	68.3%	Score 239.8	DB 1	Length 357
Best Local Similarity	82.2%	Pred. No. 2.4e-71		
Matches 290	Conservative	0	Mismatches 57	Indels 6
Gaps				
Qy	2	AGGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCACGCTGGAGGTCCTCGAGACTCT	61	
Db	2	AGGTGAAGTGTGGAGTCTGGGGAGGTCTTAGTAGGCGCTGGAGGGTCCCTCGAAACTCT	61	
Qy	62	CCTGTGCAGCCTCTGGATTTCACCTTCAGTAGCATGACATGCTTGGGTTCGCCAGGCTC	121	
Db	62	CCTGTGCAGCCTCTGGATTTCACCTTCAGTAGGATACCATGCTTGGGTTCGCCAGACTC	121	
Qy	122	CGGCAAGGCTCTGGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGGTAGCACCCTACTATT	181	
Db	122	CGGAGAAGCGCTGGAGTGGGTTCGCAACCATAGTAGTGGTGGGTGAACACCTACTATC	181	
Qy	182	TAGACACTGTGCAGGGCCGATTTCACCTCTCCAGAGACAATAGTAGAAGAACCCCTATACC	241	

[illegible]

RESULT 13
 US-08-483-199-15
 : Sequence 15, Application US/08483199
 : Patent No. 5849877
 : GENERAL INFORMATION:
 : APPLICANT: RING, DAVID B.
 : TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 : TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CHIRON CORPORATION
 : STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
 : CITY: Emeryville
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94662-8097
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/483,199
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: SAVEREIDE, PAUL
 : REGISTRATION NUMBER: 36,914
 : REFERENCE/DOCKET NUMBER: 0850.009
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (510) 601-2585
 : TELEFAX: (510) 655-3542
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 357 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 1..357
 : US-08-483-199-15

	Query Match	68.3%	Score 239.8	DB 2	Length 357
	Best Local Similarity	82.2%	Pred. No. 2.4e-71		
	Matches 290	Conservative	0	Mismatches 57	Indels 6
	Gaps				
QY	2 AGGTGCAGCTGGTGGAGTCTGGGGGAGCGGTGTGTCAGCCTGGAGCTCCCTCGAGACTCT	61			
	H				
DB	2 AGGTCAAGGTTGTGGAGTCTGGGGGAGTCTTAGTCAGGCCCTGGAGGTCCTCGAACTCT	61			
QY	62 CCTCTGCAGCCTCTGGATTACCTTCAGTATGCTATGCTCTTGGGTTGCGCAGGCTC	121			
DB	62 CCTCTGCAGCCTCTGGATTACCTTCAGTAGGTATACATGCTCTTGGGTTGCGCAGACTC	121			
QY	122 CGGCGAAGGCTCTGGAGTGGGTCCGAAAGTTACTAGTCTGGTGGTAGGACCTTACTATT	181			
DB	122 CGGAGAAGCGGCTGGAGTGGGTCCGAACCACTAGTAGTGGTGGTAGAACCACTTACTATC	181			
QY	182 TAGACACTGTGCAGGGGCCGATTCCACTCTCCAGAGACAATAGTAGAACAACCCCTATACC	241			

Db 182 CAGACAGTGTGAAGGTGCATTCCCGTCTCCAGAGACAATGCCATGAGCAGCCTGTACC 241
QY 242 TCGAATGAACCTCTCTGAGAGCCGAGGACACACCCCTGTATTACTGTGCAAGACA----- 296
Db 242 TCGAATGAGCAGTCTGAGGTCTGAGGACACGCGCTGTATTACTGTGCAAGATACGGGG 301
QY 297 -TAACCTACGGCAGTTTGTCTTACTGGGGCCAAAGGACTACAGTACTGTTTCT 348
Db 302 CTGGTGACGCGCTGGTTTGTCTTACTGGGGCCAAAGGACTCTGTGTACAGTTTCT 354

RESULT 14

US-08-484-508-15

; Sequence 15, Application US/08484508

; Patent No. 5948647

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.

; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION

; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94662-8097

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,508

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: SAVERIDE, PAUL

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0850.008

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 801-585

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..357

; US-08-484-508-15

Query Match

Best Local Similarity 68.3%; Score 239.8; DB 2; Length 357;

Matches 290; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 2 AGGTGAGTGTGGAGTCTGGGGAGGCGTGTGTCAGAGCTGGAAGGTCCCTGAGACTCT 61
Db 2 AGGTGAAGTGTGGAGTCTGGGGAGTCTTAGTAGAGGCTGGAGGTCCTGAAACTCT 61
QY 62 CCGTGTGAGCCTGTGAGTACCTTACCTAGTACTATGACATGCTTGGTTCGCCAGGCTC 121
Db 62 CCGTGTGAGCCTGTGAGTACCTTACCTAGTACTATGACATGCTTGGTTCGCCAGGCTC 121
QY 122 CGGGCAAGGCTGAGTGGTGGCGAAAAGTTAGTGTGTGTGTAGTACCACTACTATT 181
Db 122 CGGAGAGGCGGTGAGTGGTGGCGAACCATTTAGTGTGTGTGTAGTACCACTACTATC 181
QY 182 TAGACACTGTGCAGGCCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241

Db 182 CAGACAGTGTGAAGGTGCATTCCCGTCTCCAGAGACAATGCCATGAGCAGCCTGTACC 241
QY 242 TCGAATGAACCTCTCTGAGAGCCGAGGACACACCCCTGTATTACTGTGCAAGACA----- 296
Db 242 TCGAATGAGCAGTCTGAGGTCTGAGGACACGCGCTGTATTACTGTGCAAGATACGGGG 301
QY 297 -TAACCTACGGCAGTTTGTCTTACTGGGGCCAAAGGACTACAGTACTGTTTCT 348
Db 302 CTGGTGACGCGCTGGTTTGTCTTACTGGGGCCAAAGGACTCTGTGTACAGTTTCT 354

RESULT 15

US-08-053-171-10

; Sequence 10, Application US/08053171

; Patent No. 5562903

; GENERAL INFORMATION:

; APPLICANT: Co. Loibner

; TITLE OF INVENTION: Antibody Derivatives

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-54-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1..445

; OTHER INFORMATION: /standard_name= "Heavy Chain

; OTHER INFORMATION: V-region of BR55-2 Antibody in pVg-1c and pVg-3c"

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 12..425

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1..6

; OTHER INFORMATION: /standard_name= "Xba I restriction

; OTHER INFORMATION: site"

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 440..445

; OTHER INFORMATION: /standard_name= "Xba I restriction

; OTHER INFORMATION: site"

; US-08-053-171-10

Query Match

67.9%; Score 238.2; DB 1; Length 445;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:56 ; Search time 23.47 Seconds
(without alignments)
338.491 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVQLVESGGGVQPGKSLRL.....RHNYGSFAYWGQGTITVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_56: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	507	82.3	119	2	S31108	Ig heavy chain - h
2	503	81.7	119	2	C36005	Ig heavy chain v r
3	503	81.7	119	2	S31107	Ig heavy chain - h
4	503	81.7	121	2	S36666	Ig heavy chain v r
5	503	81.7	127	2	S38489	Ig heavy chain - h
6	503	81.7	140	2	S31588	Ig heavy chain v r
7	502	81.5	140	2	S31686	Ig heavy chain v r
8	501	81.3	134	2	S31679	Ig heavy chain v r
9	500.5	81.2	122	2	E36005	Ig heavy chain v r
10	499	81.0	132	2	S31603	Ig heavy chain v r
11	498.5	80.9	122	2	S31117	Ig heavy chain - h
12	498.5	80.9	128	2	S48797	Ig heavy chain v r
13	498	80.8	121	2	G36005	Ig heavy chain v r
14	494	80.2	119	2	G36005	Ig heavy chain v r
15	494	80.2	119	2	F36005	Ig heavy chain v r
16	494	80.2	123	2	S31114	Ig heavy chain - h
17	494	80.2	138	2	S31666	Ig heavy chain v r
18	493.5	80.1	120	2	S48798	Ig heavy chain v r
19	492.5	80.0	114	2	S46392	Ig heavy chain v r
20	492	79.9	117	2	S78486	Ig heavy chain v r
21	492	79.9	160	2	S05271	Ig heavy chain pre
22	491.5	79.8	114	2	S46390	Ig heavy chain v r
23	490	79.5	121	2	I55673	Ig heavy chain - h
24	488.5	79.3	137	2	S31701	Ig heavy chain v r
25	487	79.1	134	2	S31699	Ig heavy chain v r
26	485.5	78.8	118	2	S31116	Ig heavy chain - h
27	485.5	78.8	140	2	S70442	Ig heavy chain pre
28	485	78.7	133	2	A49028	Ig heavy chain v r
29	485	78.7	143	2	S23624	Ig heavy chain v r

ALIGNMENTS

RESULT 1
S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31108
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RA>
A:Cross-references: EMBL:X62956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 507; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 1.4e-39;
Matches 98; Conservative 8; Mismatches 11; Indels 2; Gaps 1;
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDSWVRQAPGKGLWYAKVSSGGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWYSAISGGSGSTYY 60
Qy 61 LDTVGRTTISRDNSKNTLYLQMNSLRAEDTAVYCA--RHNYGSFAYWGQGTITVSS 117
Db 61 ADSVKGRTTISRDNSKNTLYLQMNSLRAEDTAVYCAKDRRLTGTFDYGQGTITVSS 119

RESULT 2
C36005
Ig heavy chain v region (30p1) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571
A:Accession: C36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M18513
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

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Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 3.3e-39;
Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

QY 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGGSIYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGLVQPGSLRLSRLCAASGFTFSYAMSWVRQAPGKGLWVSAISGGGSIYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LDTVGGRFTISRDNKNTLYIQMNSLRADTAIVYICARH-NYGS-FAYWGQGTITVSS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYICAKDAGWGSGFDYWGQGTITVSS 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S31107
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAX>
A:Cross-references: EMBL:X62955
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 3.3e-39;
Matches 98; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGGSIYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGLVQPGSLRLSRLCAASGFTFSYAMSWVRQAPGKGLWVSAISGGGSIYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LDTVGGRFTISRDNKNTLYIQMNSLRADTAIVYICARHNYGS--FAYWGQGTITVSS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYICAKDAGWGSGFDYWGQGTITVSS 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Marks, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MAR>
A:Cross-references: EMBL:X61646; NID:G37688; PIDN:CAA43827.1; PID:gl335369
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 3.4e-39;
Matches 98; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY *1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGGSIYY 60
```

```
Db 1 QVQLVQSGGGVYVQPGSRSLRSLCAASGFTFSYGMHWVRQAPGKGLWVAVISYDGSNKYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LDTVGGRFTISRDNKNTLYIQMNSLRADTAIVYICARHNY---GSFAYWGQGTITVTS 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYICAKTGSSCGWGFYDWGQGTITVTS 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 S 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 S 121
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S38489
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Marks, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z23028; NID:G414025; PIDN:CAA80563.1; PID:G414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 127;
Best Local Similarity 77.2%; Pred. No. 3.6e-39;
Matches 98; Conservative 6; Mismatches 11; Indels 12; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGGSIYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGGVYVQPGSLRLSRLCAASGFTFSYAMSWVRQAPGKGLWVSAISGGGSIYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LDTVGGRFTISRDNKNTLYIQMNSLRADTAIVYICARH-----NYGSFAYWG 108
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYICAKEGFPASDYDSSGYISFDYWG 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 109 QGTTVT 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 QGTLTV 127
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S31588
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31588
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: EMBL:Z14200; NID:G30957; PIDN:CAA78569.1; PID:G30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 140;
Best Local Similarity 80.2%; Pred. No. 4e-39;
Matches 97; Conservative 11; Mismatches 9; Indels 4; Gaps 2;
```

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMSWVRQAPGKGLVWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWAKVSSGGSTYY 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVGRTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTVSS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 117 S 117
Db 140 S 140

RESULT 7
S31686
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31686
R:Cuissinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31686
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: EMBL:Z14205; NID:g30965; PIDN:CAA78574.1; PID:g30970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 502; DB 2; Length 140;
Best Local Similarity 80.2%; Pred. No. 4.9e-39;
Matches 97; Conservative 9; Mismatches 11; Indels 4; Gaps 1;
QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMSWVRQAPGKGLVWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWAKVSSGGSTYY 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVGRTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTVSS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 117 S 117
Db 140 S 140

RESULT 8
S31679
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31679
R:Cuissinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31679
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>
A:Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 501; DB 2; Length 134;
Best Local Similarity 83.8%; Pred. No. 5.8e-39;
Matches 98; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMSWVRQAPGKGLVWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKGLVWAKVSSGGSTYY 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVGRTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTVSS 134
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
E36005
Ig heavy chain V region (M72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: E36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH; IGHDY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 500.5; DB 2; Length 122;
Best Local Similarity 81.1%; Pred. No. 5.8e-39;
Matches 99; Conservative 5; Mismatches 13; Indels 5; Gaps 1;
QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMSWVRQAPGKGLVWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKGLVWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVGRTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTV 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICARHNYGSPAYWGQGTIVTV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 116 SS 117
Db 121 SS 122

RESULT 10
S31603
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31603
R:Cuissinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-113/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 499; DB 2; Length 132;
Best Local Similarity 82.1%; Pred. No. 8.6e-39;

A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34024
C:Genetics:
A:Gene: GDB:IGH; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 494; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-38;
Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGSRSLRLSCAASGFTSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60

Qy 61 LDTVGRETISRDNKNTLYLQMSLRADTAIVYICARHNYGS--FAYWGQTTVTSS 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICAKDNDNWFDPWGQTTVTSS 119

RESULT 15

F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 1
C:Accession: F36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34026
C:Genetics:
A:Gene: GDB:IGH; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 494; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 2.2e-38;
Matches 98; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
Db 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTSSYDMHWVRQAPGKLEWVAVISDGSNKYY 60

Qy 61 LDTVGRETISRDNKNTLYLQMSLRADTAIVYICARHNYGSFAY--WGQTTVTSS 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARDKASDAFDIWGQTTVTSS 119

Search completed: February 13, 2001, 09:04:13
Job time: 77 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:03:21 ; Search time 14.89 seconds
(without alignments)
253.755 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVQLVSGGGVQPGRLRL.....RHNYGSFAYWGQTTVTYSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481.5	78.2	122	1 HV3G_HUMAN	P01768 homo sapien
2	456	74.0	121	1 HV3J_HUMAN	P01771 homo sapien
3	453	73.5	119	1 HV3I_HUMAN	P01770 homo sapien
4	451.5	73.3	136	1 HV16_MOUSE	P01783 mus musculus
5	449.5	73.0	126	1 HV3K_HUMAN	P01772 homo sapien
6	446	72.4	117	1 HV3C_HUMAN	P01764 homo sapien
7	442.5	71.8	114	1 HV3B_HUMAN	P01763 homo sapien
8	441.5	71.7	116	1 HV3T_HUMAN	P01781 homo sapien
9	441.5	71.7	122	1 HV3H_HUMAN	P01769 homo sapien
10	428	69.5	117	1 HV55_MOUSE	P18526 mus musculus
11	424	68.8	115	1 HV3F_HUMAN	P01767 homo sapien
12	423	68.7	119	1 HV3L_HUMAN	P01773 homo sapien
13	418.5	67.9	116	1 HV05_CARAU	P19181 carassius a
14	418	67.9	117	1 HV54_MOUSE	P18525 mus musculus
15	415.5	67.5	119	1 HV37_MOUSE	P01807 mus musculus
16	415.5	67.5	119	1 HV40_MOUSE	P01810 mus musculus
17	415	67.4	115	1 HV3D_HUMAN	P01765 homo sapien
18	415	67.4	120	1 HV3E_HUMAN	P01766 homo sapien
19	410.5	66.6	119	1 HV3M_HUMAN	P01774 homo sapien
20	408.5	66.3	119	1 HV3N_HUMAN	P01775 homo sapien
21	407.5	66.2	120	1 HV3U_HUMAN	P01782 homo sapien
22	407.5	66.2	122	1 HV3A_HUMAN	P01762 homo sapien
23	406	65.9	117	1 HV02_CANFA	P01785 canis famil
24	405.5	65.8	114	1 HV01_CANFA	P01784 canis famil
25	404	65.6	115	1 HV32_MOUSE	P01801 mus musculus
26	403.5	65.5	119	1 HV38_MOUSE	P01808 mus musculus
27	402.5	65.3	122	1 HV20_MOUSE	P01789 mus musculus
28	402	65.3	113	1 HV30_MOUSE	P01799 mus musculus
29	400	64.9	142	1 HV01_RAT	P01805 rattus norv
30	399	64.8	118	1 HV39_MOUSE	P01809 mus musculus
31	397	64.4	113	1 HV27_MOUSE	P01796 mus musculus
32	396.5	64.4	97	1 HV56_MOUSE	P18527 mus musculus
33	395.5	64.2	111	1 HV35_MOUSE	P01804 mus musculus

RESULT 1

HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006;
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region.
FT NON_TER 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 78.2%; Score 481.5; DB 1; Length 122;
Best Local Similarity 74.6%; Pred. No. 8.9e-42;
Matches 91; Conservative 12; Mismatches 14; Indels 5; Gaps 1;

Qy 1 QVQLVSGGGVQPGRLRLCAASGFTFSYDMSWVRQAPKGLWVAKYSSGGSTYY 60
Db 1 QVELVESGGGVVQPGRLRLCAASGFTFSNYAMHWVRQPPKGLWVAVIYGBBBKYY 50
Qy 61 LDTVGRETTISRDNSKNTLYLQMSLRADETAVYYCARH-----NYGSFAYWGQTTVTY 115
Db 61 ABSYKGRETISRDNSKNTLYLQMSLRADETAVYYCARDRPLYGBYRAFNWVGQTLTV 120
Qy 116 SS 117
Db 121 SS 122

RESULT 2

HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION HIL.
OS Homo sapiens (Human).


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Query Match 73.3%; Score 451.5; DB 1; Length 136;
Best Local Similarity 74.8%; Pred. No. 1e-38;
Matches 89; Conservative 12; Mismatches 15; Indels 3; Gaps 2;

QY 2 VOLVESGGVQPGSRSLRSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTVYL 61
DB 18 VOLVESGGVQPGSRSLRSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTVYL 77
QY 62 DTVOGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQGT 117
DB 78 DTVOGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQGT 136

RESULT 5
HV3K_HUMAN
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE-83289131; PubMed-6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-81072295; PubMed-7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RN J. Mol. Biol. 141:369-391(1980).
DR PIR: A02055; G1HUKL.
DR PDB: 2FB4; 12-JUL-89.
DR PDB: 2IG2; 12-JUL-89.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin v region; 3D-structure.
FT MOD_RES 1
FT PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT TURN 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;
```

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Query Match 73.0%; Score 449.5; DB 1; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.5e-38;
Matches 90; Conservative 10; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVOLVESGGVQPGSRSLRSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 1 QVOLVESGGVQPGSRSLRSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
QY 61 LDTVOGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR---HNYGSFA-----YWGQGT 111
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR---HNYGSFA-----YWGQGT 120

QY 112 TVTVSS 117;
DB 121 PVTVSS 126;

RESULT 6
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-81101090; PubMed-6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RN Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
DR EMBL: J00236; AAA53516.1; -.
DR EMBL: M35415; AAA58735.1; -.
DR PIR: A02047; H3HU26.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 72.4%; Score 446; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.1e-38;
Matches 84; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVOLVESGGVQPGSRSLRSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 20 EVQLLESGGGLVQPGSRSLRSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 79
QY 61 LDTVOGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
DB 80 GDSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 117

RESULT 7
HV3B_HUMAN
ID HV3B_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A02046; M3HUGL.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 71.8%; Score 442.5; DB 1; Length 114;
Best Local Similarity 71.8%; Pred. No. 6.8e-38;
Matches 84; Conservative 16; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDSMSVWRQAPGKGLWVAKVSSGGSTYY 60
DB 1 QVQLVDSGGGLVPEGSLRLSCASGFTFSANDMWRQAPGKGLWLSIFGGSGSTYY 60

QY 61 LDTVGQRETIISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTVSS 117
DB 1 LDTVGQRETIISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTVSS 117

QY 61 ADSVKGRETIISRBKNSLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTVSS 117
DB 61 ADSVKGRETIISRBKNSLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTVSS 114

RESULT 8
HV3T_HUMAN STANDARD; PRT; 116 AA.
ID HV3T_HUMAN
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE=73059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete IgM-molecule."
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO THE COMPOSITION OF 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A02064; M3HUGL.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;
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Query Match 71.7%; Score 441.5; DB 1; Length 116;
Best Local Similarity 71.8%; Pred. No. 8.7e-38;
Matches 84; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDSMSVWRQAPGKGLWVAKVSSGGSTYY 60
DB 1 EVQLVESGGDLVQPGKSLRLCAASGFTFBGLGMTVWRQAPGKGLWVYANIK2BGSZZBY 60

QY 61 LDTVGQRETIISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTVSS 117
DB 61 VDSVKGRETIISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTVSS 116
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RESULT 9
HV3H_HUMAN STANDARD; PRT; 122 AA.
ID HV3H_HUMAN
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins."
RL Biochemistry 13:2482-2498(1974).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;
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Query Match 71.7%; Score 441.5; DB 1; Length 122;
Best Local Similarity 67.2%; Pred. No. 9.2e-38;
Matches 82; Conservative 19; Mismatches 16; Indels 5; Gaps 2;

QY 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDSMSVWRQAPGKGLWVAKVSSGGSTYY 60
DB 1 QVZLVZSGGAVZPGKSLRLCAASGFTSYAMHWVRQAPGKGLZWLVSISYGBBZY 60

QY 61 LDTVGQRETIISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTV 115
DB 61 AASVKGRETIISRBKNTLYLQMNSLRAEDTAVYICARHNYGSFAYWGQGTIVTV 120

QY 116 SS 117
DB 121 SS 122
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```
RESULT 10
HV55_MOUSE STANDARD; PRT; 117 AA.
ID HV55_MOUSE
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
```

RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO502; HVM334.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;

Query Match 69.5%; Score 428; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 2e-36;
Matches 80; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQVSGGGVQVQPGSRSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 20 EVQVSGGGLVQPGSLKSLCAASGFTSSYDMSVWRQPEKRLWVAIYSSGGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAVYYCAR 98
DB 80 PTVQGRFTISRDNKNTLYLQMSLRADTAVYYCAR 117

RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 68.8%; Score 424; DB 1; Length 115;
Best Local Similarity 69.2%; Pred. No. 4.9e-36;
Matches 81; Conservative 20; Mismatches 14; Indels 2; Gaps 2;

QY 1 QVQVSGGGVQVQPGSRSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 1 EVQVETGGGLIQPGSLKSLCAASGFTSSYDMSVWRQAPGKALZWVSATYR-GGTTY 59

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAVYYCARHNYGSFYAWGQGTITVTVSS 117
DB 60 ADSVKGRTISRDRSRTVYLQMSLRADTAVYYCAR-DLAAARLFQKGTITVTVSS 115

RESULT 12
HV3L_HUMAN
ID HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; A1HUBR.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 51 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28 N-LINKED (GLCNAC. .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A7534D024 CRC64;

Query Match 68.7%; Score 423; DB 1; Length 119;
Best Local Similarity 69.5%; Pred. No. 6.5e-36;
Matches 82; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

QY 1 QVQVSGGGVQVQPGSRSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 1 QVQVSGGGVQVQAGTSRLSCTSAFNLSDYAMHWVRQAPGKGLZWALISYGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAVYYCAR--HNYGSFYAWGQGTITVTVS 116
DB 61 ADSVKGRTISRDRSRTVYLQMSLRADTAVYYCAKLIYAGTRBFWGQGTITVTVS 118

RESULT 13
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.

```
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 5A.
FT CHAIN 20 116 FRAMEWORK 1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 50 54 FRAMEWORK 2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 84 FRAMEWORK 3.
FT DOMAIN 85 116 BY SIMILARITY.
FT DISULFID 41 114
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 67.9%; Score 418.5; DB 1; Length 116;
Best Local Similarity 83.7%; Pred. No. 1.8e-35;
Matches 82; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCLCAASGFTVSSNYSWVRQPPGKLEWVSVIYS-GGSTYY 78
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAIVYICAR 98
Db 79 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYICAR 116

RESULT 14
HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1999 (Rel. 16, Last sequence update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH1783 SUBFAMILY.
DR PIR: J70505; HVMS84.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 67.9%; Score 418; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 2e-35;
Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCLCAASGFTVSSNYSWVRQPPGKLEWVSVIYS-GGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAIVYICAR 98
Db 80 PDKVGRFTISRDNKNTLYLQMSLRADTAIVYICAR 117
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RESULT 15
HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR: A02077; AVMSX4.
DR HSSP: P01810; 2FBJ.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

Query Match 67.5%; Score 415.5; DB 1; Length 119;
Best Local Similarity 65.3%; Pred. No. 3.7e-35;
Matches 77; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVKLESGGGLVQPGGSLRLSCLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAIVYICAR-HNYGSFAYWGQGTFTVSS 117
Db 61 TPLSKDKFTISRDNKNTLYLQMSKVRSEDTALYTCARLHYGYAAYWGQGLTIVSA 118

Search completed: February 13, 2001, 09:23:11
Job time: 1190 sec
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NO SCALE DIVISION

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:56 ; Search time 39.42 seconds
(without alignments)
347.877 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVQVSGGVQVQGRSLRL.....RHNYGSPAYWGQTTVTSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_15:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rudent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	78.4	116	4 Q9UL93	Q9ul93 homo sapien
2	475	77.1	113	4 Q9UL90	Q9ul90 homo sapien
3	474	76.9	121	4 Q9UL71	Q9ul71 homo sapien
4	464.5	75.4	147	4 Q9Y509	Q9y509 homo sapien
5	460.5	74.8	118	4 Q9UL72	Q9ul72 homo sapien
6	460.5	74.8	122	4 Q9UL84	Q9ul84 homo sapien
7	458.5	74.4	118	4 Q9UL91	Q9ul91 homo sapien
8	419	68.0	131	4 Q9UL88	Q9ul88 homo sapien
9	414	67.2	95	4 Q9UL86	Q9ul86 homo sapien
10	403.5	65.5	298	11 Q9QXF0	Q9qxf0 mus musculu
11	403.5	65.5	437	11 Q9RIA4	Q9ria4 mus musculu
12	382.5	62.1	124	4 Q9UL92	Q9ul92 homo sapien
13	372	60.4	104	4 Q9UL87	Q9ul87 homo sapien
14	366	59.4	112	4 Q9UGP3	Q9ugp3 homo sapien
15	351.5	57.1	124	6 Q9N0W4	Q9n0w4 oryctolagus
16	349	56.7	125	4 Q9UL95	Q9ul95 homo sapien
17	348.5	56.6	124	6 Q9N0W6	Q9n0w6 oryctolagus
18	339	55.0	117	11 Q9QXE9	Q9qxe9 mus musculu
19	336.5	54.6	118	11 Q9Z1C4	Q9z1c4 mus musculu

20	333	54.1	117	11 Q9QXF0	Q9qxf0 mus musculu
21	331.5	53.8	116	4 Q9UL89	Q9ul89 homo sapien
22	325	52.8	119	4 Q9UL94	Q9ul94 homo sapien
23	317.5	51.5	109	11 Q9JL75	Q9jl75 mus musculu
24	312	50.6	119	4 Q9UL73	Q9ul73 homo sapien
25	307	49.8	157	4 Q9S978	Q9s978 homo sapien
26	306.5	49.8	110	11 Q9JL83	Q9jl83 mus musculu
27	306	49.7	150	4 Q9Y298	Q9y298 homo sapien
28	304.5	49.4	150	4 Q9S973	Q9s973 homo sapien
29	302	49.0	77	4 Q9Y741	Q9y741 homo sapien
30	297	48.2	109	11 Q9JL85	Q9jl85 mus musculu
31	296.5	48.1	110	11 Q9JL77	Q9jl77 mus musculu
32	292.5	47.5	114	11 Q9JL81	Q9jl81 mus musculu
33	292.5	47.5	122	4 Q9UL75	Q9ul75 homo sapien
34	292	47.4	82	4 Q9Y729	Q9y729 homo sapien
35	290.5	47.2	77	4 Q9Y726	Q9y726 homo sapien
36	290	47.1	117	11 Q9Z1C6	Q9z1c6 mus musculu
37	288	46.8	78	4 Q9Y730	Q9y730 homo sapien
38	286.5	46.5	77	4 Q9Y728	Q9y728 homo sapien
39	286	46.4	102	11 Q9JL79	Q9jl79 mus musculu
40	276.5	44.9	416	4 Q9NPP6	Q9npp6 homo sapien
41	274	44.5	79	4 Q9Y731	Q9y731 homo sapien
42	274	44.5	81	4 Q9Y719	Q9y719 homo sapien
43	268.5	43.6	86	4 Q9Y722	Q9y722 homo sapien
44	266	43.2	80	4 Q9Y735	Q9y735 homo sapien
45	265.5	43.1	82	4 Q9Y732	Q9y732 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9UL93	PRELIMINARY;	PRT;	116 AA.
AC	Q9UL93;			
DT	01-MAY-2000 (Tiemblrel. 13, Created)			
DT	01-MAY-2000 (Tiemblrel. 13, Last sequence update)			
DE	01-JUN-2000 (Tiemblrel. 14, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035021; AAD56257.1;			
DR	INTERPRO; IPR003006;			
DR	PFAM; PF00047; 1g; 1.			
FT	NON_TER	116		
FT	NON_TER	116		
SQ	SEQUENCE	116 AA;	12434 MW;	ODA0348154DD5061 CRC64;
Query Match : 78.4%; Score 483; DB 4; Length 116;				
Best Local Similarity 81.0%; Pred. No. 2.2e-43;				
Matches 94; Conservative 5; Mismatches 17; Indels 0; Gaps 0;				
QY	2	VQLVESGGVQVQGRSLRLSCAASGFTSSVDMKVRQAPGKLEWYAKVSGGSTYL	61	
DB	1	VQLVESGGVQVQGRSLRLSCAASGFTSSVDMKVRQAPGKLEWYAKVSGGSTYL	60	
QY	62	DTVQGRFTISRDNSKNTLYLQMNSLRADTAVYICARHNGSFAYWGQTTVTSS	117	
DB	61	DSVQGRFTISRDNSKNTLYLQMNSLRADTAVYICARHNGSFAYWGQTTVTSS	116	
RESULT	2			

Q9UL90
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1. 1
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 77.1%; Score 475; DB 4; Length 113;
Best Local Similarity 79.5%; Pred. No. 1.4e-42;
Matches 93; Conservative 6; Mismatches 14; Indels 4; Gaps 1;
QY 1 QVQLVESGGGVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
DB 1 EVQLVESGGGVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAFYDGSNKYY 60
QY 61 LDTVGQRTISRDNKNTLYLQMSLRAEDTAVYYCARHNTYSGSFAYWGQGT 117
DB 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAK-----DLNYWGQGT 113
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

RESULT 3
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -
DR HSSP; P01772; 2FB4.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1. 1
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
Query Match 76.9%; Score 474; DB 4; Length 121;
Best Local Similarity 76.0%; Pred. No. 2e-42;
Matches 92; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
DB 1 EVQLVESGGGVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAFYDGSNKYY 60
QY 61 LDTVGQRTISRDNKNTLYLQMSLRAEDTAVYYCARHNTYSGSFAYWGQGT 116
DB 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYYCAK-----DLNYWGQGT 120
QY 117 S 117
DB 121 S 121
RESULT 4
Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9607114; PubMed=7475288;
RA Cao J., Vesgio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -
DR HSSP; P01772; 2FB4.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1. 1
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 75.4%; Score 464.5; DB 4; Length 147;
Best Local Similarity 71.4%; Pred. No. 2.5e-41;
Matches 90; Conservative 9; Mismatches 18; Indels 9; Gaps 1;
QY 1 QVQLVESGGGVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
DB 1 QVHLVESGGGVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAFYDGSNKYY 60
QY 61 LDTVGQRTISRDNKNTLYLQMSLRAEDTAVYYCAR-----HNTYSGSFAYWGQGT 111
DB 61 AGSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDNVDFSVGYAGIDYWGQGT 120
QY 112 TVTVSS 117
DB 121 LVTYSS 126
RESULT 5
Q9UL72
ID Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX* MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -;
DR HSSP; P01772; 2F84.
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 118;
Best Local Similarity 78.2%; Pred. No. 5e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 3; Gaps 2;
QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTVSSNMYNVRQAPGKGLSVS-VTYSGGSYY 59
QY 61 LTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGSFA--YWGQGTFTVSS 117
Db 60 ADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYICARDRFGEFLDYWGQGTFTVSS 118

RESULT 6
Q9UL84 PRELIMINARY; PRT; 122 AA.
ID Q9UL84
AC Q9UL84;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -;
DR HSSP; P01772; 2F84.
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 122;
Best Local Similarity 73.8%; Pred. No. 5.2e-41;
Matches 90; Conservative 10; Mismatches 17; Indels 5; Gaps 1;
QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASRFTESNGMHVVRQAPGKGLVWAIISDGSNKEY 50
QY 61 LTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGS----PAYWGQGTFTV 115
Db 61 ADSVKGRTIFRDNSKNMMDLQMSLRAEDTAVYICAKDERGLVCTYFDYWGQGTFTV 120
QY 116 SS 117
Db 121 SS 122

RESULT 7
Q9UL91 PRELIMINARY; PRT; 118 AA.
ID Q9UL91
AC Q9UL91;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -;
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 74.4%; Score 458.5; DB 4; Length 118;
Best Local Similarity 76.9%; Pred. No. 8.1e-41;
Matches 90; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWYSISSTIIITY 60
QY 61 LTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARHNYG-SPAYWGQGTFTVTS 116
Db 61 ADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYICARSDSEAFDYGQGTFTVTS 117

RESULT 8
Q9UL88 PRELIMINARY; PRT; 131 AA.
ID Q9UL88
AC Q9UL88;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -;
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 68.0%; Score 419; DB 4; Length 131;
Best Local Similarity 65.6%; Pred. No. 1.3e-36;
Matches 86; Conservative 10; Mismatches 21; Indels 14; Gaps 2;

Search completed: February 13, 2001, 09:04:56
Job time: 120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:51 ; Search time 26.34 Seconds
(without alignments)
151.886 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVOLVSGGVQGRSLRL.....RHNGSFAYWGQCTTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_36:*
- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
 - 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
 - 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
 - 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
 - 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
 - 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
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 - 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
 - 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
 - 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
 - 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
 - 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
 - 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
 - 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
 - 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
 - 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
 - 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
 - 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
 - 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	117	19 W76001	Vitaxin antibody h
2	552	89.6	117	19 W76003	LM609 antibody hea
3	539	87.5	117	18 W27526	Heavy chain variab
4	539	87.5	239	20 W73874	Human antiFc epsil
5	539	87.5	242	20 W73876	Human antiFc epsil
6	536	87.0	117	20 Y06381	Murine monoclonal
7	525	85.2	130	20 Y06379	Murine monoclonal
8	523.5	85.0	118	19 W57591	Chimeric antibody
9	523.5	85.0	118	19 W89636	Human antibody hea
10	523.5	85.0	118	21 Y77512	Peptide seq ID No:
11	523.5	85.0	137	19 W57603	Chimeric antibody
12	523.5	85.0	137	20 W89635	Human antibody hea

13	523.5	85.0	137	21 Y77514	Peptide encoded by
14	517.5	84.0	139	15 R52823	Humanised murine K
15	517.5	84.0	139	16 R70471	Humanised anti-KC-
16	517.5	84.0	240	20 Y02472	A single chain ant
17	517	83.9	121	20 W86122	Protein sequence o
18	509.5	82.7	139	18 W21652	Humanised reshaped
19	509	82.6	240	21 Y15124	Anti-human CTLA-4
20	509	82.6	240	21 Y15125	Anti-murine CTLA-4
21	508	82.5	121	20 W86120	Protein sequence o
22	508	82.5	138	21 Y32406	Mouse anti-verotox
23	505	82.0	113	19 W70621	Human consensus fr
24	505	82.0	113	19 Y82347	Human consensus se
25	503.5	81.7	443	18 W13564	Humanised anti-L-S
26	503	81.7	117	20 W86137	Protein sequence o
27	502	81.5	119	14 R32240	Humanised Mab heav
28	501.5	81.4	120	18 W27553	Human Ab heavy cha
29	501.5	81.4	281	18 W27560	Consensus single c
30	500.5	81.2	131	18 W13520	Anti-melanoma anti
31	500.5	81.2	143	21 Y82829	Human PTHrp monocl
32	500	81.2	117	19 W48866	Chimeric humanized
33	500	81.2	117	20 W86135	Protein sequence o
34	500	81.2	264	19 W73049	Humanised A33 scab
35	500	81.2	532	19 W73051	233dCH2.z chimeric
36	500	81.2	643	19 W73050	233g2C237Az chimer
37	497.5	80.8	122	15 R50311	Humanised heavy ch
38	497.5	80.8	122	15 R50315	Humanised heavy ch
39	497.5	80.8	143	21 Y82621	Human PTHrp monocl
40	496.5	80.6	118	18 W06208	Xenograft antibody
41	496.5	80.6	120	19 W23952	Chimeric humanised
42	496.5	80.6	240	19 W23954	Chimeric humanised
43	496	80.5	117	16 R79157	Human IgE receptor
44	496	80.5	119	13 R23739	Recombinant heavy
45	496	80.5	119	14 R41721	Aglycosylated anti

ALIGNMENTS

RESULT 1

ID W76001 standard; Protein; 117 AA.

XX AC W76001;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; Integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49820.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX anglogenesis or restenosis

PS Claim 1; Fig 1a; 129pp; English.

XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 100.0%; Score 616; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.5e-49;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPKGLVWAKVSSGGSTYY 60
 Db 1 qvqlvesgggvvqpgksrlslscasgftfssydmsswvrqapkglewakvssgggstyy 60

QY 61 LDTVGRTISRDNSKNTLYIQMNSLRADTAVYICARHNYGSPAYWGQGTIVTVSS 117

Db 61 ldtvggrftisrdnsnkntlyiqmnslnsraedtavyycarhnygsfaywgqgtvtvss 117

RESULT 2

W76003
 ID W76003 standard; Protein; 117 AA.

XX AC W76003;

XX DT 02-NOV-1998 (first entry)

XX LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI: 1998-437472/37.

XX DR N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX

CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 89.6%; Score 552; DB 19; Length 117;
 Best Local Similarity 88.0%; Pred. No. 1.1e-43;
 Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPKGLVWAKVSSGGSTYY 60
 Db 1 evqlvesgggvlvqpgksrlslscasgftfssydmsswvrqipeklewkvssgggstyy 60

QY 61 LDTVGRTISRDNSKNTLYIQMNSLRADTAVYICARHNYGSPAYWGQGTIVTVSS 117

Db 61 ldtvggrftisrdnsnkntlyiqmnslnsraedtavyycarhnygsfaywgqgtltvsa 117

RESULT 3

W27526

ID W27526 standard; Protein; 117 AA.

XX AC W27526;

XX DT 16-DEC-1997 (first entry)

XX Heavy chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX OS Homo sapiens.

XX PN JP09191886-A.

XX PD 29-JUL-1997.

XX PF 19-JAN-1996; 96JP-0024816.

XX PR 19-JAN-1996; 96JP-0024816.

XX PA (ASAK) ASahi BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHIIN KK.

XX PA (TSUR/) TSURA T.

XX DR WPI: 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IgE receptor - useful medicinally and have low

XX antigenicity in humans

XX Claim 2; Page 13; 26pp; Japanese.

XX The present sequence, the heavy chain variable region of the human
 CC antibody (Ab) CRA2, was used in the preparation of a humanised or
 CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
 CC determining regions (CDR) from a murine, anti-human high affinity
 CC immunoglobulin E (IgE) receptor MAb. The humanised, semi-chimeric
 CC or chimeric MAb can be used to treat or prevent diseases, and has very
 CC specifically allergies, associated with the receptor, and has very

CC low antigenicity in humans.

XX Sequence 117 AA;

Query Match 87.5%; Score 539; DB 18; Length 117;

Best Local Similarity 86.3%; Pred. No. 1.6e-42;

Matches 101; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAKVSSGGSTYY 60

DB 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAFISNRGGSTYY 60

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 61 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 117

RESULT 4

W73874

ID W73874 standard; Protein; 239 AA.

XX AC W73874;

DT 31-MAR-1999 (first entry)

DE Human antiFc epsilon RI alpha chain antibody #2.

KW AntiFc epsilon RI alpha chain antibody; antibody production; human.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "signal peptide"

FT Protein 20..239

FT Protein /note= "mature protein"

XX PN JP11000174-A.

XX PD 06-JAN-1999.

XX PF 13-JUN-1997; 97JP-0171232.

XX PR 13-JUN-1997; 97JP-0171232.

XX PA (ASAK) ASAH I BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHI N KK.

XX PA (TSUR/) TSURA T.

XX DR WPI; 1999-124394/11.

XX DR N-PSDB; X01214.

PT Preparing an antibody Fab fragment using yeast - in high yield

XX PS Claim 6; Page 7; 13pp; Japanese.

CC This sequence represents a human antiFc epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast Pichia pastoris as the host cell. The method can prepare an antibody Fab fragment cost efficiently and in high yield.

XX SQ Sequence 239 AA;

Query Match 87.5%; Score 539; DB 20; Length 239;

Best Local Similarity 86.3%; Pred. No. 3.6e-42;

Matches 101; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAKVSSGGSTYY 60

DB 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAFISNRGGSTYY 60

DB 20 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAFISNRGGSTYY 79

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 80 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 136

RESULT 5

W73876

ID W73876 standard; Protein; 242 AA.

XX AC W73876;

DT 31-MAR-1999 (first entry)

DE Human antiFc epsilon RI alpha chain antibody #4.

KW AntiFc epsilon RI alpha chain antibody; antibody production; human.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..22

FT Protein /note= "signal peptide"

FT Protein 23..242

FT Protein /note= "mature protein"

XX PN JP11000174-A.

XX PD 06-JAN-1999.

XX PF 13-JUN-1997; 97JP-0171232.

XX PR 13-JUN-1997; 97JP-0171232.

XX PA (ASAK) ASAH I BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHI N KK.

XX PA (TSUR/) TSURA T.

XX DR WPI; 1999-124394/11.

XX DR N-PSDB; X01216.

PT Preparing an antibody Fab fragment using yeast - in high yield

XX PS Claim 6; Page 9-10; 13pp; Japanese.

CC This sequence represents a human antiFc epsilon RI alpha chain antibody, produced using the method of the invention. The method is for preparing an antibody Fab fragment using the yeast Pichia pastoris as the host cell. The method can prepare an antibody Fab fragment cost efficiently and in high yield.

XX SQ Sequence 242 AA;

Query Match 87.5%; Score 539; DB 20; Length 242;

Best Local Similarity 86.3%; Pred. No. 3.6e-42;

Matches 101; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAKVSSGGSTYY 60

DB 23 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLWVAFISNRGGSTYY 82

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 83 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 139

RESULT 6

Y06381

ID Y06381 standard; Protein; 117 AA.

XX

PA (CHUS) CHUGAI SEIYAKU KK.
 XX Sato K, Tsunenari T;
 XX WPI: 2000-117115/10.
 DR
 XX Treatment of hypercalcaemic crisis with a substance inhibiting binding
 of parathyroid hormone related peptide to its receptor
 PT
 XX Example 4; Page 95-96; 120pp; Japanese.
 PS
 XX The invention relates to a method of treatment of hypercalcaemic crisis.
 CC A composition for the treatment of hypercalcaemic crisis contains as
 CC active component a substance which inhibits the binding of parathyroid
 CC hormone related peptide (hPTHrP) to its receptor. The inhibitor is used
 CC for the treatment of hypercalcaemic crisis, such as that associated with
 CC a malignant tumour.
 XX
 XX Sequence 118 AA;
 SQ

Query Match 85.0%; Score 523.5; DB 21; Length 118;
 Best Local Similarity 87.3%; Pred. No. 4.3e-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
 QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMQSVWVROAPKGLVWAKVSSGGSTYY 60
 DB 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMQSVWVROAPKGLVWAKVSSGGSTYY 60
 QY 61 LDTVQGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGS-FAYWGQGTFTVSS 117
 DB 61 pdsvkgrftisrdnsknltlylqmnsraedtavyycarqgtmttyfaywgqgtltvss 118

RESULT 11
 W57603
 ID W57603 standard; Protein; 137 AA.
 XX
 AC W57603;
 XX
 DT 03-SEP-1998 (first entry)
 XX
 DE Chimeric antibody fragment against hPTHrP SEQ ID NO:58.
 XX
 KW Chimeric; antibody; human parathormone related peptide; hPTHrP; mouse;
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KW hypophosphatemia; pathogen; vitamin D resistance; V region; C region;
 KW humanised.
 XX
 OS Synthetic.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal
 XX
 PN WO9813388-A1.
 XX
 PD 02-APR-1998.
 XX
 PF 24-SEP-1997; 97WO-JP03382.
 XX
 PR 24-JUL-1997; 97JP-0214168.
 PR 26-SEP-1996; 96JP-0255196.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Sato K, Wakahara Y, Yabuta N;
 XX WPI: 1998-230640/20.
 DR N-PSDB; V24243.
 XX

PT New chimeric antibodies against human parathormone related
 PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
 PT disorders caused by malignant neoplasm(s)
 XX
 XX Claim 60; Page 122-123; 182pp; Japanese.
 PS
 XX New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTHrP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphatemia such as that due to
 CC pathogens or to vitamin D resistance.
 XX
 XX Sequence 137 AA;
 SQ

Query Match 85.0%; Score 523.5; DB 19; Length 137;
 Best Local Similarity 87.3%; Pred. No. 5.1e-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
 QY 1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMQSVWVROAPKGLVWAKVSSGGSTYY 60
 DB 20 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYDMQSVWVROAPKGLVWAKVSSGGSTYY 79
 QY 61 LDTVQGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGS-FAYWGQGTFTVSS 117
 DB 80 pdsvkgrftisrdnsknltlylqmnsraedtavyycarqgtmttyfaywgqgtltvss 137

RESULT 12
 W89635
 ID W89635 standard; Protein; 137 AA.
 XX
 AC W89635;
 XX
 DT 14-APR-1999 (first entry)
 XX
 DE Human antibody heavy chain protein.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KW inhibitor; humanised.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal
 FT Protein 20..137
 XX
 PN WO9851329-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 13-MAY-1998; 98WO-JP02116.
 XX
 PR 18-JUL-1997; 97JP-0194445.
 PR 15-MAY-1997; 97JP-0125505.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Ishii K, Sato K, Tunenari T;
 XX WPI: 1999-070101/06.
 DR N-PSDB; X00116.
 XX
 PT Inhibitors of binding of parathyroid hormone related peptide to its
 PT receptor - useful for, e.g. treatment of cachexia arising from

PT cancer or other diseases

Example 4; Page 83-84; 125pp; Japanese.

The present invention describes compositions for the treatment of cachexia containing a substance which inhibits the binding of a parathyroid hormone related peptide (PTHrP) to its receptor, as an active component. This substance may be an antagonist to the receptor, or an antibody (preferably monoclonal), or antibody fragment, or recognising PTHrP. The antibody is preferably humanised or chimeric. The present invention also describes a humanised antibody prepared by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for the treatment of cachexia arising in connection with diseases such as cancer, thereby improving the quality of life of the patient. The present sequence represents a human antibody heavy chain from the present invention.

XX Sequence 137 AA;

Query Match 85.0%; Score 523.5; DB 20; Length 137;
Best Local Similarity 87.3%; Pred. No. 5.1e-41;
Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
DB 20 qvqlvesgggvvqpgksrlslscasgftfssygmwvrqapkglewatisggsgsty 79
QY 61 LDTVOGRTTISRDNSKNTLYIQMNSLRADTAHYICARHNYGS-FAYWGQGTITVSS 117
DB 80 pdsvkgrftisrdnskntlyiqmnsraedtavvyrcargttmtfyayvgggtltvss 137

RESULT 13

Y77514
ID Y77514 standard; Protein; 137 AA.

XX AC Y77514;

DT 26-APR-2000 (first entry)

XX Peptide encoded by DNA seq ID No: 58.

DE Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.

XX KW Homo sapiens.

XX OS WO200000219-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-JP03433.

XX PR 26-JUN-1998; 98JP-0180143.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Tsunenari T;

XX WPI; 2000-117115/10.

DR N-PSDB; 258914.

XX Treatment of hypercalcemic crisis with a substance inhibiting binding

PT of parathyroid hormone related peptide to its receptor

XX Example 4; Page 98-99; 120pp; Japanese.

XX The invention relates to a method of treatment of hypercalcemic crisis.
CC A composition for the treatment of hypercalcemic crisis contains as
CC active component a substance which inhibits the binding of parathyroid
CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
CC for the treatment of hypercalcemic crisis, such as that associated with
CC a malignant tumour.

XX Sequence 137 AA;

Query Match 85.0%; Score 523.5; DB 21; Length 137;
Best Local Similarity 87.3%; Pred. No. 5.1e-41;
Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
DB 20 qvqlvesgggvvqpgksrlslscasgftfssygmwvrqapkglewatisggsgsty 79
QY 61 LDTVOGRTTISRDNSKNTLYIQMNSLRADTAHYICARHNYGS-FAYWGQGTITVSS 117
DB 80 pdsvkgrftisrdnskntlyiqmnsraedtavvyrcargttmtfyayvgggtltvss 137

RESULT 14

R52823
ID R52823 standard; Protein; 139 AA.

XX AC R52823;

DT 25-JAN-1995 (first entry)

XX Humanised murine KC-4 immunoglobulin heavy chain V-region.

XX Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human mammary fat globule; human breast carcinoma;
KW murine anti-HMFG monoclonal antibody KC-4; humanised analogue.

XX OS Chimeric Mus musculus.

XX OS Chimeric Homo sapiens.

XX PN WO9411509-A.

XX PD 26-MAY-1994.

XX PF 16-NOV-1993; 93WO-US11445.

XX PR 16-NOV-1992; 92US-0977696.

XX PR 30-SEP-1993; 93US-0129930.

XX PR 08-OCT-1993; 93US-0134346.

XX PA (CANC-) CANCER RES FUND CONTRA COSTA.

XX PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;

XX WPI; 1994-183510/22.

XX DR N-PSDB; Q62804.

XX New analogue peptide(s) comprising antibody variable regions -

PT used to develop prods. for use in the detection, diagnosis,

PT therapy and prevention of neoplasms

XX Example 75; Page 95; 109pp; English.

XX This sequence represents a humanised murine anti-human carcinoma

CC KC-4 antibody heavy chain variable region. The humanised antibody is

CC useful for carcinoma therapy and diagnosis and for in vivo imaging

CC of neoplastic cells. It is also of use in inhibiting the growth of

CC a primary or metastasised neoplasm.

XX Sequence 139 AA;

Query Match 84.0%; Score 517.5; DB 15; Length 139;
Best Local Similarity 83.3%; Pred. No. 1.8e-40;
Matches 100; Conservative 6; Mismatches 11; Indels 3; Gaps 1;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
DB 20 eqvnmvsgggivqpggslrlscasgftafssygmwvrqapkglewaeissggnvay 79

Search completed: February 13, 2001, 09:03:47
Job time: 56 sec

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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:52 ; Search time 18.5 Seconds
(without alignments)
113.566 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 636
Sequence: 1 QVQLVESGGGVQPGKSLRL.....RHNYGSPAYWGQGTIVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/1aa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.5	84.0	139	1 US-08-129-930B-96	Sequence 96, Appl
2	505	82.0	113	3 US-08-974-899-6	Sequence 6, Appl
3	503.5	81.7	443	4 PCT-US96-13152-4	Sequence 4, Appl
4	502.5	81.6	122	2 US-07-934-373C-21	Sequence 21, Appl
5	502.5	81.6	122	3 US-08-437-642B-21	Sequence 21, Appl
6	502.5	81.6	122	4 PCT-US93-07832-21	Sequence 12, Appl
7	502	81.5	119	1 US-08-053-171-12	Sequence 99, Appl
8	502	81.5	125	1 US-08-478-039-99	Sequence 99, Appl
9	502	81.5	125	1 US-08-478-349A-99	Sequence 99, Appl
10	500.5	81.2	131	3 US-08-983-607-28	Sequence 28, Appl
11	497.5	80.8	122	4 PCT-US93-08435-12	Sequence 12, Appl
12	497.5	80.8	122	4 PCT-US93-08435-43	Sequence 43, Appl
13	496	80.5	119	1 US-07-988-925-11	Sequence 11, Appl
14	496	80.5	119	2 US-08-362-780-11	Sequence 11, Appl
15	495	80.4	119	1 US-08-331-388A-46	Sequence 46, Appl
16	495	80.4	119	2 US-08-331-397B-46	Sequence 46, Appl
17	495	80.4	119	2 US-08-759-804A-46	Sequence 46, Appl
18	495	80.4	119	4 PCT-US94-07659-6	Sequence 6, Appl
19	494.5	80.3	117	1 US-07-942-245-36	Sequence 36, Appl
20	494.5	80.3	122	4 PCT-US93-08435-14	Sequence 14, Appl
21	494	80.2	120	1 US-07-942-245-35	Sequence 35, Appl
22	494	80.2	125	2 US-08-428-197-1	Sequence 1, Appl
23	494	80.2	125	4 PCT-US93-10555-1	Sequence 1, Appl
24	492.5	80.0	116	3 US-08-983-607-36	Sequence 36, Appl
25	491	79.7	123	2 US-08-665-202-30	Sequence 30, Appl
26	489.5	79.5	120	2 US-07-934-373C-4	Sequence 4, Appl
27	489.5	79.5	120	3 US-08-437-642B-4	Sequence 4, Appl
28	489	79.4	119	1 US-08-207-996-22	Sequence 22, Appl

US-08-129-930B-96
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/POCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-96

ALIGNMENTS

RESULT 1

US-08-129-930B-96
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/POCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-96

Query Match 84.0%; Score 517.5; DB 1; Length 139;
Best Local Similarity 83.3%; Pred. No. 6.7e-46;
Matches 100; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 20 EVQVLESGLVQPGKSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 79
Qy 61 LDTVGGRFTISRDNKNTLYLQMNSLRADTAIVYICARHNYGS---FAYWGQGTIVTVSS 117
Db 80 QDTVTGRTISRDNKNTLYLQMNSLRADTAIVYICAREDYGIPAWFAYWGQGTIVTVSS 139

RESULT 2

US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-974-899-6

Query Match 82.0%; Score 505; DB 3; Length 113;
Best Local Similarity 83.8%; Pred. No. 9.9e-45;
Matches 98; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGLVQPGKSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Qy 61 LDTVGGRFTISRDNKNTLYLQMNSLRADTAIVYICARHNYGSFAYWGQGTIVTVSS 117
Db 61 ADSVKGRTISRDNKNTLYLQMNSLRADTAIVYICAR----GFDYWGQGTIVTVSS 113

RESULT 3

PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 81.7%; Score 503.5; DB 4; Length 443;
Best Local Similarity 83.8%; Pred. No. 6.9e-44;
Matches 98; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGLVQPGKSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSSGGSTYY 59
Qy 61 LDTVGGRFTISRDNKNTLYLQMNSLRADTAIVYICARHNYGSFAYWGQGTIVTVSS 117
Db 60 PDSVKGRTISRDNKNTLYLQMNSLRADTAIVYICARDYDGDYWGQGTIVTVSS 116

RESULT 4
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:

; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

RESULT 6
PCT-US93/07832-21
; Sequence 21, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: .patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:

```

REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-21

Query Match 81.6%; Score 502.5; DB 4; Length 122;
Best Local Similarity 80.3%; Pred No. 1.9e-44;
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLWEVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSVMWRQAPGKGLWEVSVISGDSSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LTVGGRFTISRDNSKNTLYLQMNSLRADTAIVYCARHNY-----GSFAYWGQGTIVTV 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVGRFTISRDNSKNTLYLQMNSLRADTAIVYCARGRVGLSGLDYWGQGTIVTV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 116 SS 117
||
Db 121 SS 122

RESULT 7
US-08-053-171-12
; Sequence 12, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Sequence of Humanized

; Patent No. 5562903
; OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant
; OTHER INFORMATION: H-hu-BR55-2/1"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 31..35
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 50..66
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 99..108
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; US-08-053-171-12

Query Match 81.5%; Score 502; DB 1; Length 119;
Best Local Similarity 81.5%; Pred No. 2.1e-44;
Matches 97; Conservative 13; Mismatches 7; Indels 2; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLWEVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSYDMYVWRQAPGKGLWEVAYISGGSSHY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LTVGGRFTISRDNSKNTLYLQMNSLRADTAIVYCAR-HNYGS-FAYWGQGTIVTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VDSVGRFTISRDNSKNTLYLQMNSLRADTAIVYCARHNYGS-FAYWGQGTIVTVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-08-478-039-99
; Sequence 99, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raad, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-478-039-99

Query Match 81.5%; Score 502; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 2.2e-44;
Matches 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNWVRQAPGKLEWVAKVSSGGSTYY 60
DB 1 EYQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKLEWVYXISGGSTYY 60
QY 61 LDTVQGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARHN---YGSFAY-----WQGGTT 112
DB 61 ADSVKGRFTISRDDSKNTLYLQMSLRAEDTAVYYCAKGVLYYSGSYHWEDPWQGGTL 120
QY 113 VTVSS 117
DB 121 VTVSS 125

RESULT 9
US-08-476-349A-99
Sequence 99, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: Teskit Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-476-349A-99

Query Match 81.5%; Score 502; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 2.2e-44;
Matches 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNWVRQAPGKLEWVAKVSSGGSTYY 60
DB 1 EYQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKLEWVYXISGGSTYY 60
QY 61 LDTVQGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARHN---YGSFAY-----WQGGTT 112
DB 61 ADSVKGRFTISRDDSKNTLYLQMSLRAEDTAVYYCAKGVLYYSGSYHWEDPWQGGTL 120
QY 113 VTVSS 117
DB 121 VTVSS 125

RESULT 10
US-08-983-607-28
Sequence 28, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544

TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scfv antibodies obtained from
LIBRARY: fUSE5 fusion phage construct
CLONE: V13
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-28

Query Match 81.2%; Score 500.5; DB 3; Length 131;
Best Local Similarity 82.1%; Pred. No. 3.4e-44;
Matches 96; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMQWVRQAPGKGLWEVAKVSSGGSTYY 60
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLWEVSAISGGSTYY 60
QY 61 LDTVGRTTISRDNKNTLYLQMSLRAEDTAVYYCARHNYGSFAYWGQGTFTVYSS 117
DB 61 ADSVKGRTTISRDNKNTLYLQMSLRAEDTAVYYCAK-GVAPEDYWGQGTFTVYSS 116

RESULT 11
PCT-US93-08435-12
Sequence 12, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-12

Query Match 80.8%; Score 497.5; DB 4; Length 122;
Best Local Similarity 79.5%; Pred. No. 6.3e-44;
Matches 97; Conservative 9; Mismatches 11; Indels 5; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMQWVRQAPGKGLWEVAKVSSGGSTYY 60
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLWEVSEISDGGSTYY 60
QY 61 LDTVGRTTISRDNKNTLYLQMSLRAEDTAVYYCAR---HNYGSFA--TWGQGTFTTV 115
DB 61 PDTVTGRTTISRDNKNTLYLQMSLRAEDTAVYYCAKLIYYGYDGYAMDYWGQGTFTV 120
QY 116 SS 117
DB 121 SS 122

RESULT 12
PCT-US93-08435-43
Sequence 43, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-43

Db 1 EYOLBSGGELVQPGSURLSCAASGTFSSFPMAWVRQAPGKLEWSTISTSGRTYY 60

QY 61 LDTVOGRFTISRDNSKNLTLYLQMSLRAEDTAVYICA--RHNYGSFAYWGQGTTVTVSS 117
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Db 61 RDSVKGRFTISRDNSKNLTLYLQMSLRAEDTAVYICAKFRQYSGGFDYNGQGTFLTVSS 119

RESULT 14

US-08-362-780-11

; Sequence 11, Application US/08362780

; Patent No. 5968509

; GENERAL INFORMATION:

; APPLICANT: Gorman, Scott D

; APPLICANT: Routledge, Edward G

; APPLICANT: Waldmann, Herman

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye pc
STREET: 8th Floor, 1100 No. 5968509th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,780
FILING DATE:

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RESULT 15
US-08-331-398A-46
Sequence 46, Application US/08331398A

Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match 80.4%; Score 495; DB 1; Length 119;
Best Local Similarity 81.5%; Pred. NO. 1.1e-43;
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Db 1 QVELVESGGVVPQGRSLRLSCAASGFTFSYAMHWVRQAPGKGLVWAVISYDGSNKYY 60
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Db 61 ADVKGRFTISRDNSKNTLYLQMNSLRADTAVYICARSRATYYFDWGQTLVTSS 119

Search completed: February 13, 2001, 09:03:16
Job time: 24 sec.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 09:13:00 ; Search time 1535.21 Seconds
(without alignments)
1070.080 Million cell updates/sec

Title: US-08-790-540A-3
Perfect score: 321
Sequence: 1 GAGATTGCTACTACTCAGTC.....GGACCAAGGTGGAANTTAAG 321

Scoring table: IDENTITY_NUC
Gapex 10.0, Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_ba2.*
3: gb_om.*
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5: gb_ph.*
6: gb_pl1.*
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8: gb_pr1.*
9: gb_pr2.*
10: gb_pr3.*
11: gb_ro.*
12: gb_sy.*
13: gb_un.*
14: em_fun.*
15: em_hum1.*
16: em_hum2.*
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76: em_htg10.*
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84: gb_htg24.*
85: gb_pr8.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	247.2	77.0	321	11	MUSCMVF	M95943 Mouse mRNA
2	247.2	77.0	321	11	MUSIGKACY	M35667 Mouse lysoz
3	247.2	77.0	370	11	MUSIGKXD	M93959 Mouse Ig ac
4	245.6	76.5	321	11	AF163757	AF163757 Mus muscu
5	245.6	76.5	321	11	MUSCMVH	M95945 Mouse mRNA
6	245.6	76.5	381	81	E07933	E07933 CDNA encodi
7	245.6	76.5	381	81	I31959	I31959 Sequence 82
8	245.6	76.5	381	82	I78571	I78571 Sequence 82
9	245.6	76.5	381	82	I78626	I78626 Sequence 82
10	245.6	76.5	431	11	MUSIGKCNJ	M19913 Mouse Ig re
11	244.4	76.1	324	11	AF139844	AF139844 Mus muscu
12	244.4	76.0	324	11	AF139849	AF139849 Mus muscu
13	244.4	76.0	330	11	MUSIGL2VK	L78684 Mus musculu
14	242.4	75.5	324	11	AF139845	AF139845 Mus muscu
15	242.4	75.5	324	11	AF139846	AF139846 Mus muscu
16	242.4	75.5	381	11	AF045514	AF045514 Mus muscu
17	242.4	75.5	582	11	MMU26998	U26998 Mus musculu
18	242.4	75.5	738	11	MMU40581	U40581 Mus musculu
19	240.8	75.0	321	11	AF13242	AF13242 Mus muscu
20	240.8	75.0	321	11	AF13243	AF13243 Mus muscu
21	240.8	75.0	321	11	MMU27215	AJ27215 Mus muscu

22 240.8 75.0 321 11 MMU27216 Mus muscu
23 240.8 75.0 324 11 AF139847 Mus muscu
24 240.8 75.0 324 11 AF139848 Mus muscu
25 240.8 75.0 348 11 MMU16070
26 240.4 74.9 324 11 MMU60469
27 239.6 74.6 420 11 MUSIGKCKN
28 239.6 74.6 5238 81 AF087031
29 239.2 74.5 324 11 AF087031
30 238.6 74.3 317 11 MMIGIKL4
31 238 74.1 317 11 MMIGIKL3
32 235 73.2 313 11 MUSIGVABU
33 234.6 73.1 321 11 MMU16181
34 234.4 73.0 381 11 MUSIGKAQA
35 234.2 73.0 307 11 AF139235
36 234 72.9 313 11 MUSIGVABW
37 233.8 72.8 318 11 MMIGKVR4
38 233.6 72.8 323 11 MMUNTDNAF
39 233.2 72.6 306 11 MMIGLT91
40 233.2 72.6 315 11 MMU88691
41 232.8 72.5 300 11 MUSIGKABY
42 232.8 72.5 321 11 MMALCVR26
43 232 72.3 318 11 MMU88689
44 231.2 72.0 324 11 MMU16184
45 230.2 71.7 303 11 S66242 anti-myelin

ALIGNMENTS

RESULT 1
MUSCMVF MUSCMVF 321 bp mRNA ROD 26-JUL-1993
DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95943
VERSION M95943.1 GI:309175
KEYWORDS
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S.,
Co.M.S., Vasquez, M., Britt, W.J. and Coelinhg, K.L.
TITLE Unpublished (1992)
JOURNAL
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="Mab 33"
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mat_peptide 1..321
/note="putative"
BASE COUNT 86 a 81 c 74 g 80 t
ORIGIN

Query Match 77.0%; Score 247.2; DB 11; Length 321;
Best Local Similarity 85.3%; Pred. No. 2.le-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGGCGACT 60
DB 1 GATATTGTGCTAACTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCACT 60
QY 61 CTTTCTGCGAGCCAGGCAAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
DB 61 CTTTCTGCGAGCCAGGCAAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
QY 121 GGTCAAGCCCAAGCGTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
DB 121 GGTCAAGCCCAAGCGTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGCTCTGGAGCGCT 240
DB 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGCTCTGGAGCGCT 240
QY 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTAAACAGTGGCCCGTACACGTTCCGAGGG 300
DB 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTAAACAGTGGCCCGTACACGTTCCGAGGG 300

Db 121 CATGAGTCTCCAAGCTTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCTCC 180
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DB 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCTCTCACTATCAACAGTGTGGAGACT 240
QY 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTGGCAGCTGGCCTCACTACACGTTCCGAGGG 300
DB 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTAAACAGTGGCCTCATACGTTCCGAGGG 300
QY 301 GGGACCAAGTGGAAATTA 320
DB 301 GGGACCAAGTGGAAATTA 320
RESULT 2
MUSIGKACY MUSIGKACY 321 bp mRNA ROD 27-APR-1993
LOCUS Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
DEFINITION mRNA, partial cds.
ACCESSION M35667
VERSION M35667.1 GI:196584
KEYWORDS immunoglobulin light chain; immunoglobulin-kappa; processed gene;
variable region VK23.
SOURCE Mouse hybridoma, cDNA to mRNA, clone 10K-106.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and
Brooks, W.B.R.
TITLE A three-dimensional model of an anti-lysozyme antibody
JOURNAL J. Mol. Biol. 194, 713-724 (1987)
MEDLINE 88011212
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
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BASE COUNT 88 a 80 c 75 g 78 t
ORIGIN
Query Match 77.0%; Score 247.2; DB 11; Length 321;
Best Local Similarity 85.3%; Pred. No. 2.le-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCTCAGCCACCCTGTCTCTCAGCCAGGAGAGGGCGACT 60
DB 1 GATATTGTGCTAACTCTCAGCCACCCTGTCTGTGACTCCAGGAAATAGCGTCACT 60
QY 61 CTTTCTGCGAGCCAGGCAAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
DB 61 CTTTCTGCGAGCCAGGCAAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
QY 121 GGTCAAGCCCAAGCGTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
DB 121 GGTCAAGCCCAAGCGTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGCTCTGGAGCGCT 240
DB 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGCTCTGGAGCGCT 240
QY 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTAAACAGTGGCCCGTACACGTTCCGAGGG 300
DB 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTAAACAGTGGCCCGTACACGTTCCGAGGG 300

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QY 301 GGGACCAAGGTGGAATAA 320
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Db 301 GGGACCAAGGTGGAATAA 320

RESULT 3
MUSIGKXD 370 bp mRNA ROD 27-APR-1993
LOCUS Mouse Ig active kappa-chain V-region, partial cds.
DEFINITION M93959
ACCESSION M93959
VERSION M93959.1 GI:197572
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Takeda,Y., Wise,K.S. and Hoffman,R.W.
JOURNAL Nucleotide sequences of immunoglobulin heavy and light chain
MEDLINE V-regions from a monoclonal autoantibody specific for a unique set
FEATURES of small nuclear ribonucleoprotein complexes
Nucleic Acids Res. 20, 4099-4099 (1992)
92375706
source Location/Qualifiers
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BASE COUNT 96 a 90 c 86 g 98 t
ORIGIN

Query Match 77.0%; Score 247.2; DB 11; Length 370;
Best Local Similarity 85.3%; Pred. No. 2.1e-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
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Db 37 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAAGTCAGT 96
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QY 61 CTTTCTCTGCAGCGCCAGCAAAAGTATTAGCAACCACTACCTGGTATCAACAAGGCCT 120
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Db 97 CTTTCTCTGCAGCGCCAGCAAAAGTATTAGCAACCACTACCTGGTATCAACAAGGCCT 156
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QY 121 GGTCAAGCCCCAAGGCTTCTATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGCC 180
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Db 157 CATGAGTCTCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 216
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QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300
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Db 277 GAAGATTTTGGAGTATTTCTGTCAACAGAGTAAACAGCTGGCCTCATACGTTCCGATCG 336
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QY 301 GGGACCAAGGTGGAATAA 320

Query Match 76.5%; Score 245.6; DB 11; Length 321;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

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Db 301 GGGACCAAGGTGGAATAA 320

RESULT 4
AF163757 321 bp mRNA ROD 04-AUG-1999
LOCUS Mus musculus mab 101.4.1 immunoglobulin light chain variable region
DEFINITION mRNA, partial cds.
ACCESSION AF163757
VERSION AF163757.1 GI:5690320
KEYWORDS house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 321)
JOURNAL Mertens,N.M., Galvin,J.E., Adderson,E.E. and Cunningham,M.W.
AUTHORS Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
TITLE Mouse Monoclonal Antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Mertens,N.M. and Cunningham,M.W.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
City, OK 73190, USA
FEATURES Location/Qualifiers
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KLEIK"
BASE COUNT 83 a 83 c 73 g 82 t
ORIGIN

Query Match 76.5%; Score 245.6; DB 11; Length 321;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
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Db 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCAGT 60
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QY 61 CTTTCTCTGCAGCGCCAGCAAAAGTATTAGCAACCACTACCTGGTATCAACAAGGCCT 120
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Db 61 CTTTCTCTGCAGCGCCAGCAAAAGTATTAGCAACCACTACCTGGTATCAACAAGGCCT 120
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QY 121 GGTCAAGCCCCAAGGCTTCTATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGCC 180
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Db 121 CATGAGTCTCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
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QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCAGTCTCCAGTCTGGAGCCT 240
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Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCTCTCAGTATCAACAGTCTGGAGCCT 240
|||
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300
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Db 241 GAAGATTTTGGAGTATTTCTGTCAACAGAGTAAACAGCTGGCCTCTACGTTCCGATCG 300
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QY 301 GGGACCAAGGTGGAATAA 320
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Db 301 GGGACCAAGGTGGAATAA 320
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RESULT 5
MUSCMVH 321 bp mRNA ROD 26-JUL-1993
LOCUS Mouse mRNA sequence, partial cds.
DEFINITION M95945
ACCESSION M95945.1 GI:309177
KEYWORDS Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S.,
Co.M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L.
TITLE Untitled
JOURNAL Unpublished (1992)
FEATURES
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            /organism="Mus musculus"
            /strain="BALB/c"
            /sub_species="domesticus"
            /db_xref="taxon:10090"
            /cell_line="MAB 5"
            /cell_type="hybridoma"
            /note="putative"
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            mat_peptide
BASE COUNT 85 a 79 c 77 g 80 t
ORIGIN

Query Match 76.5%; Score 245.6; DB 11; Length 321;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGTCTAAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGAAAGGGGACT 60
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DB 1 GATATTGTCTAAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGATAGCGTCACT 60
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QY 61 CTTTCTGCGAGCGGAGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCT 120
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DB 61 CTTTCTGCGAGCGGAGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCT 120
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
|||
DB 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 180
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QY 181 AGGTTTCAGTGGGATCGAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240
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DB 181 AGGTTTCAGTGGGATCGAGGACAGATTTACCTCTCACTGTCAACGGTGTGGAGCT 240
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QY 241 GAAGATTTGCGAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCACAGTTCCGAGGG 300
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DB 241 GAAGATTTGGAATGATTTCTGTCAACAGAGTAAAGTGGCCTCATACGTTCCGAGGG 300
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QY 301 GGGACCAAGGTGGAAATTA 320
|||
DB 301 GGGACCAAGGTGGAAATTA 320
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RESULT 6
E07933 381 bp RNA PAT 29-SEP-1997
LOCUS CDNA encoding variable region of mouse anti-FHV-1 antibody L chain.
DEFINITION E07933
ACCESSION E07933.1 GI:2176065
KEYWORDS JP 1994217786-A/2.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 381)
AUTHORS Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y.

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TITLE ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT
JOURNAL ENCODING THE SAME ANTIBODY
COMMENT Patent: JP 1994217786-A 2 09-AUG-1994;
        CHEMO SERO THERAPEUT RES INST
        OS Mus.sp. (mouse)
        PN JP 1994217786-A/2
        PD 09-AUG-1994
        PF 28-NOV-1992 JP 1992341255
        PI KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO, PI
        TOKIYOSHI YUKIO
        PC C12P21/08.A61K39/395.C07K15/00.C12N15/13.(C12P21/08.C12R1:91);
        CC strandedness: Double;
        CC topology: Linear;
        CC hypothetical: No;
        CC anti-sense: No;
        FH Key Location/Qualifiers
        FH source 1..381
        FT /organism="Mus sp."
        FT 1..381
        FT /product="variable region of mouse anti-FHV-1
        FT antibody L
        FT chain"
        FT Location/Qualifiers
        source 1..381
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        BASE COUNT 94 a 98 c 86 g 103 t
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Query Match 76.5%; Score 245.6; DB 81; Length 381;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

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DB 61 GATATTGTCTAAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGATAGCGTCACT 120
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QY 61 CTTTCTGCGAGCGGAGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCT 120
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DB 121 CTTTCTGCGAGCGGAGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCT 120
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
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DB 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 240
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QY 181 AGGTTTCAGTGGGATCGAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240
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DB 241 AGGTTTCAGTGGGATCGAGGACAGATTTCACTCTCACTGTCAACAGTGTGGAGCT 300
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QY 241 GAAGATTTGCGAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCACAGTTCCGAGGG 300
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DB 301 GAAGATTTGGAATGATTTCTGTCAACAGAGTAAAGTGGCCTCATACGTTCCGAGGG 360
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QY 301 GGGACCAAGGTGGAAATTA 320
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DB 361 GGGACCAAGGTGGAGCTGNA 380
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RESULT 7
I31959 381 bp DNA PAT 06-FEB-1997
LOCUS Sequence .82 from patent US 5585089.
DEFINITION I31959
ACCESSION I31959.1 GI:1822750
VERSION I31959.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 381)
AUTHORS Queen,C.I. and Selick,H.E.
TITLE Humanized immunoglobulins

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JOURNAL Patent: US 5585089-A 82 17-DEC-1996;

FEATURES Location/Qualifiers

1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

Query Match 76.5%; Score 245.6; DB 81; Length 381;

Best Local Similarity 85.0%; Pred. No. 6.4e-64;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60

DB 61 GATATTGTGCTAACTAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCACT 120

QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCGT 120

DB 121 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAATCA 180

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180

DB 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGTCC 240

QY 181 AGGTTCAAGGCGAGTGGATCAGGAGCAGATTTACCCCTCACTATCTCCAGTCTGGAGCGT 240

DB 241 AGGTTCAAGTGGAGTGGATCAGGAGCAGATTTCACTCTCAAGCTGTCAACGGTGTGGAGCT 300

QY 241 GAAGATTTTGGAGTGTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGG 300

DB 301 GAAGATTTTGGAGTGTATTCTGTCAACAGATACAGTTGGCTTCATACGTTTCGGAGG 360

QY 301 GGGACCAAGCTGGAAATTA 320

DB 361 GGGACCAAGCTGGAAATTA 380

RESULT 8

I78571

LOCUS

I78571 381 bp DNA PAT 03-APR-1998

DEFINITION Sequence 82 from patent US 5693761.

ACCESSION

I78571

VERSION I78571.1 GI:3014725

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 381)

AUTHORS

Queen,C.L., Schneider,W.P. and Selick,H.E.

TITLE

Polynucleotides encoding improved humanized immunoglobulins

JOURNAL

Patent: US 5693761-A 82 02-DEC-1997;

FEATURES

Location/Qualifiers

1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

/organism="unknown"

Query Match

Best Local Similarity 76.5%; Score 245.6; DB 82; Length 381;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60

DB 61 GATATTGTGCTAACTAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCACT 120

QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCGT 120

DB 121 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAATCA 180

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180

DB 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGTCC 240

QY 181 AGGTTCAAGTGGAGTGGATCAGGAGCAGATTTACCCCTCACTATCTCCAGTCTGGAGCGT 240

DB 241 AGGTTCAAGTGGAGTGGATCAGGAGCAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300

QY 241 GAAGATTTTGGAGTGTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGG 300

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QY 301 GGGACCAAGCTGGAAATTA 320

DB 361 GGGACCAAGCTGGAAATTA 380

RESULT 9

I78626

LOCUS

I78626 381 bp DNA PAT 03-APR-1998

DEFINITION Sequence 82 from patent US 5693762.

ACCESSION

I78626

VERSION I78626.1 GI:3014780

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 381)

AUTHORS

Queen,C.L., Co.M.Sung, Schneider,W.P., Landolfi,N.F., Coelinhg,K.L.

TITLE

Humanized immunoglobulins

JOURNAL

Patent: US 5693762-A 82 02-DEC-1997;

FEATURES

Location/Qualifiers

1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

/organism="unknown"

Query Match

Best Local Similarity 76.5%; Score 245.6; DB 82; Length 381;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60

DB 61 GATATTGTGCTAACTAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCACT 120

QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAATCA 180

DB 121 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAATCA 180

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180

DB 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGTCC 240

QY 181 AGGTTCAAGTGGAGTGGATCAGGAGCAGATTTACCCCTCACTATCTCCAGTCTGGAGCGT 240

DB 241 AGGTTCAAGTGGAGTGGATCAGGAGCAGATTTCACTCTCAGTGTCAACGGTGTGGAGCT 300

QY 241 GAAGATTTTGGAGTGTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGG 300

DB 301 GAAGATTTTGGAGTGTATTCTGTCAACAGAGTACAGTTGGCTTCATACGTTTCGGAGG 360

QY 301 GGGACCAAGCTGGAAATTA 320

DB 361 GGGACCAAGCTGGAAATTA 380

RESULT 10

MUSIGKCNJ

LOCUS

MUSIGKCNJ 431 bp mRNA ROD 26-MAR-1994

DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone AN1K.

ACCESSION

M19913 J03832

VERSION M19913.1 GI:197033

KEYWORDS

C-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.


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QY 181 AGTTCAGTGGCAGTGCATCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
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QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCACAGTTCGAGGG 300
Db 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCACAGTTCGAGGG 300
QY 301 GGGACCAAGCTGGAATAA 320
Db 301 GGGACCAAGCTGGAATAA 320

RESULT 12
AF139849
LOCUS AF139849 324 bp mRNA ROD 04-NOV-1999
DEFINITION Mus musculus clone 38 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
ACCESSION AF139849
VERSION AF139849.1 GI:4732162
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 324)
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
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            /strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
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            265..291
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            /note="CDR3; complementarity determining region 3"
            287..324
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ORIGIN

Query Match 76.0%; Score 244; DB 11; Length 324;
 Best Local Similarity 84.7%; Pred. No. 2e-63;
 Matches 271; Conservative 2; Mismatches 47; Indels 0; Gaps 0;

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QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGCAGCT 60
Db 1 GATATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTGACTCCAGGAGATAGCGTCAGT 60
QY 61 CTTTCTGTCAGCCAGCCAGCAAGTATTAGCAACCACCTACACTGGTATCAACAAGGCCT 120
Db 61 CTTTCTGTCAGCCAGCCAGCAAGTATTAGCAACCACCTACACTGGTATCAACAAGGCCT 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180
Db 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGATCCCGCC 180
QY 181 AGTTCAGTGGCAGTGCATCAGGACAGATTTCACCTCACATATCTCCAGTCTGGAGCCT 240
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QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCACAGTTCGAGGG 300
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Db 301 GGGACCAAGCTGGAATAA 320

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RESULT 13

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MUSIGL2VK
LOCUS MUSIGL2VK 330 bp DNA ROD 17-JUN-1996
DEFINITION Mus musculus (isolate 3D7.2VK) immunoglobulin light chain (Igl-V)
chain, partial variable region.
ACCESSION L78684
VERSION L78684.1 GI:1374935
KEYWORDS immunoglobulin light chain; variable region.
SOURCE Mus musculus (individual isolate 3D7.2VK, strain MRL-LPR/LPR) DNA.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 330)
AUTHORS Gilkeson,G.S., Lefkowitz,J.B. and Di Valerio,R.
TITLE Murine glomerulotrophic monoclonal antibodies are highly
oligoclonal and exhibit distinctive molecular features
JOURNAL J. Immunol. (1996) In press
FEATURES
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            89 a 80 c 77 g 84 t
BASE COUNT 89 a 80 c 77 g 84 t
ORIGIN

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Best Local Similarity 84.7%; Pred. No. 2e-63; 2; Mismatches 47; Indels 0; Gaps 0;
Matches 271; Conservative 2;

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1 GATATTGTCTAACTCAGTCTCCAGCCACCCCTGTCTGTGACTCCAGGAGATAGTCACT 60

misc_feature
61 CTTTCTGCGAGCCAGCCAGCAAGATATTAGCAACCCCTACACTGCTGTATCAACAAGGCT 120
|||
61 CTTTCTGCGAGCCAGCCAGCAAGATATTAGCAACCCCTACACTGCTGTATCAACAAGGCT 120

misc_feature
121 GGTCAAGCCGCCAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGGC 180
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121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTGTGGCATCCCTCC 180

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181 AGTTCAGTGGCAGTGGATCAGGACAGATTTACCTTCACTCTCATTATCAACAGTGTGGAGCT 240
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181 AGTTCAGTGGCAGTGGATCAGGACAGATTTACCTTCACTCTCATTATCAACAGTGTGGAGCT 240

misc_feature
241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCCACAGTTCGGAGGG 300
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301 GGGACCAAGGTGGAATTA 320

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BASE COUNT      86 a      75 g      81 t
ORIGIN

Query Match          75.5%; Score 242.4; DB 11; Length 324;
Best Local Similarity 84.4%; Pred. No. 6e-63; 2; Mismatches 48; Indels 0; Gaps 0;
Matches 270; Conservative 2;

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DB 1 GATATTGTCTAACTCAGTCTCCAGCCACCCCTGTCTGTGACTCCAGGAGATAGTCACT 60

QY 61 CTTTCTGCGAGCCAGGCGAGCAAGTATTAGCAACCCCTACACTGCTGTATCAACAAGGCT 120
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DB 61 CTTTCTGCGAGGCGAGCAAGTATTAGCAACCCCTACACTGCTGTATCAACAAGGCT 120

QY 121 GGTCAAGCCGCCAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGGC 180
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DB 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTGTGGCATCCCTCC 180

QY 181 AGTTCAGTGGCAGTGGATCAGGACAGATTTACCTTCACTCTCATTATCAACAGTGTGGAGCT 240
|||
DB 181 AGTTCAGTGGCAGTGGATCAGGACAGATTTACCTTCACTCTCATTATCAACAGTGTGGAGCT 240

QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCCACAGTTCGGAGGG 300
|||
DB 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCTCCACAGTTCGGAGGG 300

QY 301 GGGACCAAGGTGGAATTA 320
|||
DB 301 GGGACCAAGGTGGAATTA 320

RESULT 15
AF139846 324 bp mRNA ROD 04-NOV-1999
LOCUS AF139846
DEFINITION Mus musculus clone 15 immunoglobulin kappa light chain variable region VK23 (196) mRNA, partial cds.
ACCESSION AF139846
VERSION AF139846.1 GI:4732156
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard, F., Shannon, M., Prak, E.L., Litwin, S. and Weigert, M.
TITLE Somatic mutation and light chain rearrangement generate autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard, F. and Weigert, M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University, Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
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gene
CDS
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Query Match 75.5%; Score 242.4; DB 11; Length 324;
Best Local Similarity 84.4%; Pred. No. 6e-63;
Matches 270; Conservative 2; Mismatches 48; Indels 0; Gaps 0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 08:47:13 ; Search time 1450.07 Seconds
(without alignments)
1551.238 Million cell updates/sec

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Perfect score: 321
Sequence: 1 GAGATTGCTACTCAGTC.....GGACCAAGGTGGAATTAAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:
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5: gb_est5:
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7: gb_est7:
8: gb_est8:
9: gb_est9:
10: gb_est10:
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37: gb_est37:
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39: gb_est39:
40: gb_est40:
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42: em_estfun:
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44: em_esthum2:
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114: em_esthum23:
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116: em_estom2:

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189: em_estpl78:*

190: gb_gss25:*
191: gb_gss26:*
192: gb_gss27:*
193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205.6	64.0	434	90	AW406486 UI-HF-BL0
2	204.4	63.7	398	90	AW405309 UI-HF-BL0
3	201.2	62.7	519	90	AW405183 UI-HF-BL0
4	200.8	62.6	385	90	AW405025 UI-HF-BL0
5	199.6	62.2	468	90	AW405643 UI-HF-BL0
6	199.2	62.1	624	106	BE306691 601104076
7	198	61.7	468	90	AW404506 UI-HF-BL0
8	196.4	61.2	465	90	AW404697 UI-HF-BL0
9	192	59.8	330	90	AW406212 UI-HF-BL0
10	191.6	59.7	514	90	AW405207 UI-HF-BL0
11	191.6	59.7	615	97	AW959456 EST371526
12	191.4	59.6	461	90	AW406219 UI-HF-BL0
13	189.4	59.0	413	90	AW406440 UI-HF-BL0
14	188.4	58.7	409	90	AW406057 UI-HF-BL0
15	186.8	58.2	443	90	AW405460 UI-HF-BL0
16	186.8	58.2	448	90	AW404726 UI-HF-BL0
17	185.6	57.8	708	106	BE309445 601095331
18	185.4	57.8	317	90	AW404261 UI-HF-BL0
19	185	57.6	504	90	AW405787 UI-HF-BL0
20	183.4	57.1	369	90	AW405943 UI-HF-BL0
21	181.8	56.6	518	90	AW406576 UI-HF-BL0
22	181.8	56.6	644	90	AW405817 UI-HF-BL0
23	181.2	56.4	473	90	AW406934 UI-HF-BL0
24	180.4	56.2	425	90	AW406785 UI-HF-BL0
25	180	56.1	604	90	AW405198 UI-HF-BL0
26	179.8	56.0	408	90	AW404674 UI-HF-BL0
27	179.4	55.9	489	90	AW406154 UI-HF-BL0
28	178.6	55.6	395	97	AW951626 EST363711
29	178.6	55.6	424	38	AV661282 AV661282
30	178.6	55.6	433	38	AV647117 AV647117
31	178.6	55.6	440	38	AV647111 AV647111
32	178.6	55.6	544	90	AW405216 UI-HF-BL0
33	178.6	55.6	793	38	AV646708 AV646708
34	178.4	55.6	487	89	AW378557 PMO-HT022
35	178.4	55.6	534	92	AW579665 PM2-HT022
36	178.2	55.5	354	90	AW406043 UI-HF-BL0
37	177.6	55.3	355	90	AW405010 UI-HF-BL0
38	177.2	55.2	423	90	AW406796 UI-HF-BL0
39	177	55.1	661	38	AV693657 AV693657
40	177	55.1	686	38	AV698744 AV698744
41	177	55.1	690	38	AV687177 AV687177
42	174.4	54.3	311	90	AW405931 UI-HF-BL0
43	174.2	54.3	412	38	AV695569 AV695569
44	173.6	54.1	336	90	AW407282 UI-HF-BL0
45	172.6	53.8	427	90	AW406386 UI-HF-BL0

ALIGNMENTS

RESULT: 1
AW406486 434 bp mRNA
LOCUS UI-HF-BL0-acr-f-12-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060238 5', mRNA sequence.
ACCESSION AW406486
VERSION AW406486.1 GI:6925543
KEYWORDS EST, human.
SOURCE

DEFINITION UI-HF-BL0-acb-b-10-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058506 5', mRNA sequence.
ACCESSION AW405183
VERSION AW405183.1 GI:6924240
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 519)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058506"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 127 a 153 c 126 g 112 t 1 others
ORIGIN

Query Match 62.7%; Score 201.2; DB 90; Length 519;
Best Local Similarity 76.6%; Pred No. 1.9e-51;
Matches 245; Conservative 1; Mismatches 74; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAATCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
DB 23 GAAATTGTGTGACACAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACC 82
QY 61 CTTTCTCCAGCCAGCCAGCAAGTATTAGCACACCACCTACACTGTGTATCAACAAGGCT 120
DB 83 CTCTCTCCAGCCAGCCAGGCTCTCTATGTATGATCCAGCCAGGCACTGGCATCCAGCC 142
QY 121 GGTCAGCCAGCCAGGCTCTCTATCMKKTATCTCTCCAGTCCATCTCTGGGATCCCGCC 180
DB 143 GCGCAGGCTCCAGGCTCTCTATGTATGATCCAGCCAGGCACTGGCATCCAGCC 202
QY 181 AGGTTTCAGTGGCAGTATGATGAGGAGAGATTTACCCCTACATCTCTCAGTCTGGAGCT 240
DB 203 AGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCTCAGCAGCCTAGAGCT 262
QY 241 GAAGATTTGCACTTATTACTGTCAACAGAGTGGCAGCTGGCTTCACAGCTTCGGAGG 300
DB 263 GAAGATTTTACAGTTTATTACTGTGACAGCGTAGCAACTGGCTCCGACGTTGGGCAA 322
QY 301 GGGACCAAGGTGGAATTA 320
DB 323 GGGACCAAGGTGGAATCA 342

RESULT 4
AW405025
LOCUS
DEFINITION UI-HF-BL0-abx-e-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058252 5', mRNA sequence.
ACCESSION AW405025
VERSION AW405025.1 GI:6924082
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 385)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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1..385
Location/Qualifiers
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 88 a 114 c 98 g 85 t
ORIGIN

Query Match 62.6%; Score 200.8; DB 90; Length 385;
Best Local Similarity 76.7%; Pred No. 2.3e-51;
Matches 244; Conservative 1; Mismatches 73; Indels 0; Gaps 0;
QY 3 GATTGTGCTAATCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACTCT 62
DB 7 GATTGTGTGTACAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACCCT 66
QY 63 TTCTTCAGCCAGCCAGCCAGCAAGTATTAGCAACCACTACACTGTGTATCAACAAGGCGCTG 122
DB 67 CTCTTCAGCCAGCCAGTCCAGAGTGTTCGAGTACTTAGCTGTGTACCAACAAGGCGCTG 126
QY 123 TCAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCCAG 182
DB 127 CCAGGCTCCAGGCTCTCATCTATGATGATCAACAGGCGCACTGGCATCCAGCCAG 186
QY 183 GTTCAGTGGCAGTGGATCAGGAGACAGATTTCCACCTCTACTATCTCCAGTCTGGAGCTGA 242
DB 187 GTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGACCTTAGAGCTGA 246
QY 243 AGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTTCACAGCTTCGGAGGGG 302
DB 247 AGATTTTGCAGTCTATTACTGTGACGAGGAGCGACTGGCTCGGAGCTTCGCGCAAGG 306
QY 303 GACCAAGGTGGAATTA 320
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Db	221	AGTTTCAGTGGCAGTGGGCTGGACAGACTTCACTCTCACCATCAGCAGCCTTAGAGCCT	280
QY	241	GAAGATTTCAGTCTATTACTCTCAACAGAGTGGCAGTGGCCTCACAGTTTCGGAGG	300
Db	281	GAAGATTTCAGTCTATTACTCTCAGCAGCGTAGCAACTGGTTGTACAGCTTTTGGCCAG	340
QY	301	GGACCAAGTGGAAATTA	320
Db	341	GGACCAAGCTGGAGATCAA	360

RESULT 8

AW404697

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW404697

UI-HP-BLJ-acd-b-04-0-UI.r1 NIH_MGC_37 Homo sapiens CDNA clone

IMAGE:3058518 5', mRNA sequence.

AW404697

AW404697.1 GI:6923754

EST

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 465)

NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

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/clone="IMAGE:3058518"

/clone_lib="NIH_MGC_37"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (UT1)"

/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT

108 a 139 c 115 g 103 t

ORIGIN

Query Match

Best Local Similarity 61.2%; Score 196.4; DB 90; Length 465;

Matches 242; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

QY	1	GAGATTCGCTAACTAGTCTCAGCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGCAGCT	60
Db	85	GAATATGATGACCGAGTCTCAGCCACCTGTCTGTCTCCAGGGGAAAGAGCCACC	144
QY	61	CTTTCGSCAGGCCAGCCCAAGATTATAGCAACCACTACACCTGGTATCAACAAGAGCCT	120
Db	145	CTCTCTGCGAGGGCCAGTCAGAGTGTAGCAACAACCTTAGCCCTGGTACCAGCAGAAACCT	204
QY	121	GGTCAAGCCCGAGGCTTCATCMKKATATCGTTCAGTCCAGTCCATCTCTGGATCCCGGCC	180
Db	205	GGCAGGCTCCGAGGCTCCCTCATCTATGTTGGTGCATCCACAGGGGCCACTGTATCCAGCC	264


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Db 145 CTCCTCTGCAGGCCAGTCAGAGTGTAGCAGCAACTTAGCCTGTGTACAGCAGAAATCT 204
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 205 GCCCAGGCTCCAGGCTCTCATCTAATGTTGATCCAGGCGCAGTGTATCCAGCC 264
QY 181 AGGTTTCAGTGGCAGTGGATTCAGGAGCAGATTTACAGCTTACAGCTTCCAGTGTGGAGCCT 240
Db 265 AGGTTTCAGTGGCAGTGGGCTCTGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCT 324
QY 241 GAAGATTTTCAGTGTATTACTGTGCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 325 GAAGATTTTCAGTGTATTACTGTGCAACAGAGTGGCAGTGTATTAAGTGGCCTCGGACGTTTCGCCAA 384
QY 301 GGGACCAAGGTGGAATTA 320
Db 385 TGGACCAAGGTGGAATCA 404

RESULT 11
LOCUS AW959456 615 bp mRNA EST 01-JUN-2000
DEFINITION EST371526 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION AW959456
VERSION AW959456.1 GI:8149140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Hegde,P., Qi,R.A., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 133
Seq primer: Reverse.
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
/note="Vector: pBluescriptSKM"
BASE COUNT 162 a 181 c 140 g 132 t
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Best Local Similarity 74.7%; Pred. No. 1.8e-48;
Matches 239; Conservative 1; Mismatches 80; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCTGTCTCTCAGCCCGCAGGAGAGGCGACT 60
Db 52 GAAATAGTGATCAGCAGTCTCCAGCCACCTATCTGTCTCCAGGGAAGAGCCACC 111
QY 61 CTTTCTGCCAGCCAGCAAGTATTAGCACCACCTACACTGTGTATCAACAGGCT 120
Db 112 CTCCTCTGTAGGCGCAGTATAGCAGCAACTTAGCCTGTGTATCAGCAGAACT 171
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 172 GCCCAGGCTCCAGGCTCTCATCTAATGTTGATCCAGGCGCAGTGTATCCAGCC 231
QY 181 AGGTTTCAGTGGCAGTGGATTCAGGAGCAGATTTACCCCTCACTATCTCCAGTGTGGAGCCT 240

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Db 232 AGGTTTCAGTGGCAGTGGTCTGGGACAGAGTACACTCTCACATCAGCAGCTGCAGTCT 291
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Db 292 GAAGATTTTCAGTGTATTACTGTCAACAGAGTGGCAGTGTATTAAGTGGCCTCGGACGTTTCGCCAA 351
QY 301 GGGACCAAGGTGGAATTA 320
Db 352 GGGACCAAGGTGGAATCA 371

RESULT 12
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DEFINITION UI-HF-BL0-acp-b-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059684 5', mRNA sequence.
ACCESSION AW406219
VERSION AW406219.1 GI:6925276
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 461)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
ECO RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 103 a 136 c 117 g 105 t
ORIGIN
Query Match 59.6%; Score 191.4; DB 90; Length 461;
Best Local Similarity 76.5%; Pred. No. 1.9e-48;
Matches 247; Conservative 1; Mismatches 72; Indels 3; Gaps 1;
QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCTGTCTCTCAGCCCGCAGGAGAGGCGACT 60
Db 29 GAATTTGTGTACACAGTCTCCAGCCACCTGTCTTGTCTCCAGGGAAGAGCCACC 88
QY 61 CTTTCTGCCAGCCAGCAGCAAGTATTAGCAACACCTTACACTGTGTATCAACAAAGGCT 120
Db 89 CTCCTCTGCAGGCGCAGTGTGTAGCAGTACTTAGCCTGTGTATCCACAGAAACT 148
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGGCC 180

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Db 149 GGCACGGCTCCAGGCTCCTCAFTTATGATGATCAATCAACAGGGCCACTGGCGTCCAGCC 208
QY 181 AGGTTCAAGTGGAGTCAAGGACAGATTTTCAACCTCACTATCTCCAGTCTGGAGCCT 240
Db 209 AGGTTCAAGTGGAGTGGGCTGGACAGACTTCACTCTACCACTAGAGCCT 268
QY 241 GAAGATTTTGCAGTCTATCTACTCAACAGAGTGGAGCTGGCCT---CACAGTTCGGA 297
Db 269 GAAGATTTTGCAGTCTATCTACTCAACAGAGTGGAGCTGGCCTCCCTCACTTTCGGC 328
QY 298 GGGGGACCAAGGTGGAATTA 320
Db 329 GGAGGACCAAGGTGAGATCAA 351

RESULT 13
LOCUS AW406440 413 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BL0-ach-b-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3060038 5', mRNA sequence.
ACCESSION AW406440
VERSION AW406440.1 GI:6925497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
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1. .413
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/lab_host="DH10B (LTI)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 92 a 122 c 103 g 96 t
ORIGIN
Query Match 59.0%; Score 189.4; DB 90; Length 413;
Best Local Similarity 77.1%; Pred. No. 7.6e-48;
Matches 229; Conservative 1; Mismatches 67; Indels 0; Gaps 0;
QY 24 AGCCACCTGCTCTCAGCCAGGAGAGGGGAGTCTTTCTGCGAGGCCAGCCAAAG 83
Db 8 AGCCACCTGCTCTTCTCCAGGGAGAGCCACCTCTCTGCGAGGCCAGTCCAG 67
QY 84 TATTAGAACACCTACACTGGTATCAACAAAGCCTGGTCAAGCCCAAGGCTTCTCAT 143
Db 68 TATTAGCAGTACTTAGCCTGTACCAGCAGAAACCTGGCCAGGCTCCCGAGGCTCTCTCAT 127
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QY 144 CMKKTATCGITCCAGTCCATCTCTGGGATCCCGCCAGGTTCAAGTGGCAGTGCATCAGG 203
Db 128 CTATGATACATCACACGGCCACTGGCATCCAGCCAGGTTCAAGTGGCAGTGGTCTGG 187
QY 204 GACAGATTTTCAAGTCACTATCTCCAGTCTGGAGCCTGAAGATTTTGCAGTCTATCTAG 263
Db 188 GACAGATTTTCACTCTCAACATCAGCAGCCTAGAGCTGAAGATTTTGCAGTCTATCTAG 247
QY 264 TCAACAGAGTGGCAGTGGCCTCACAGTTCGAGGGGGGACCAAGTGGAAATTA 320
Db 248 TCAGCAGCGTAGCACTGGCTCTCACTTTGGCGGAGGTCACAGTGGAGATCAA 304

RESULT 14
LOCUS AW406057 409 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BL0-ach-d-12-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059014 5', mRNA sequence.
ACCESSION AW406057
VERSION AW406057.1 GI:6925149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
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/db_xref="taxon:9606"
/clone_image="IMAGE:3059014"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 93 a 119 c 107 g 90 t
ORIGIN
Query Match 58.7%; Score 188.4; DB 90; Length 409;
Best Local Similarity 74.1%; Pred. No. 1.5e-47;
Matches 237; Conservative 1; Mismatches 82; Indels 0; Gaps 0;
QY 1 GAGATTTGCTCACTCACTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGGACT 60
Db 36 GAAATAGTGAATGATGAGTCTCCAGCCACCTGTCTGTCTCTCCAGGGGAGAGCCACC 95
QY 61 CTTTCTTCGAGCCGAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCT 120
Db 96 CTCCTCTGAGGGCCAGTCAGAGTGTAGCAGCACTAGCCTGGTACCAGCAGAACT 155
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NO SIGNATURE REQUIRED

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 09:56:38 ; Search time 103.87 Seconds
(without alignments)
1160.949 Million cell updates/sec

Title: US-08-790-540A-3

Perfect score: 321

Sequence: 1 GAGATTGCTACTACAGTC.....GGACCAAGGTGGAAATTAAG 321

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N_Geneseq 36:*
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 - 2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT:*
 - 3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT:*
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 - 21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	319.8	99.6	321	19 V49843	LM609 antibody lig
2	318.6	99.3	321	19 V49821	Vitaxin antibody 1
3	265.8	82.8	321	19 V49823	LM609 antibody lig
4	258.4	80.5	381	21 V35244	Humanised anti-ver
5	250.4	78.0	321	20 V71800	Humanised anti-alp
6	250.4	78.0	338	20 V71802	Vitronectin alpha
7	245.6	76.5	381	15 O64167	Sequence of mouse
8	239.6	74.6	5238	11 O04654	Plasmid pBT111 enc
9	239.2	74.5	324	20 V71798	Murine vitronectin
10	232.8	72.5	381	21 V35242	Mouse anti-verotox
11	229.6	71.5	416	18 T49345	cDNA encoding kapp
12	228	71.0	324	17 T33446	EGF receptor chime

13	223.6	69.7	486	14	Q43245	hIL2R Ab L chain V
14	223.6	69.7	8858	20	Z10202	Expression vector
15	222	69.2	363	17	T38510	Light chain coding
16	216.6	67.5	315	20	V71803	JK gene segment.
17	216.6	67.5	315	20	V71805	Humanised anti-alp
18	214	66.7	321	20	Z10203	DNA encoding the v
19	213.6	66.5	322	15	O44714	Light chain variab
20	213.6	66.5	322	20	Z28545	Light chain variab
21	209.2	65.2	321	20	Z10205	DNA encoding the v
22	205.6	64.0	322	14	Q36615	Anti-IL2R-beta ant
23	205.6	64.0	1395	10	N90300	Insert coding for
24	204	63.6	321	14	Q43243	B-B10 Mab L chain
25	204	63.6	321	19	V26766	Anti-gp54 MAB 48-1
26	204	63.6	486	14	Q43384	L-chain V-region o
27	202.8	63.2	642	20	X77408	Anti-human TNF- α p
28	202.4	63.1	381	18	T49338	cDNA encoding kapp
29	202.4	63.1	416	18	T49344	cDNA encoding kapp
30	202.4	63.1	416	18	T49342	cDNA encoding kapp
31	201	62.6	318	14	Q48766	Monoclonal antibod
32	200.8	62.6	381	19	V12262	Monoclonal antibod
33	199.8	62.2	720	19	V26770	Anti-gp54 MAB 48-1
34	199.2	62.1	794	17	T42033	Plasmid pMW152-225
35	199.2	62.1	2070	17	T42035	Plasmid pSW202-225
36	199.2	62.1	2793	17	T42039	Plasmid pMS238-5-2
37	199.2	62.1	2793	17	T42040	Plasmid pMS238-225
38	199.2	62.1	3177	17	T42041	Plasmid pMS240-5-2
39	198.8	61.9	318	19	V54788	DNA encoding the l
40	198.8	61.9	720	19	V54790	scFv comprising he
41	196.4	61.2	720	14	Q40462	Fv(TU27). Homo sa
42	194.4	60.6	717	14	Q40463	Fv(TU25). Homo sa
43	193.8	60.4	429	18	T70811	Mouse anti-idiotyp
44	193.4	60.2	300	13	Q20306	B cell hybridoma 1
45	191.2	59.6	321	18	T87441	Humanised cA2 ligh

ALIGNMENTS

RESULT 1

V49843
ID V49843 standard; DNA; 321 BP.

XX V49843:

DT 02-NOV-1998 (first entry)

DE LM609 antibody light chain variable region DNA grafted fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.

XX Mus sp.

XX Key Location/Qualifiers

FT CDS 1..321

FT /tag- a

FT /product- "LM609 grafted antibody light chain variable region"

FT /note- "partial sequence, no start or stop codon given"

FT WO9833919-A2

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

```

PI Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
DR P-PSDB; W76006.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis.
XX Claim 24; Fig 7; 129pp; English.
XX This sequence encodes a LM609 grafted antibody variable light chain
CC region. LM609 and the antibody vitaxin bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
CC and thus block integrin-mediated signal transduction. This is useful in
CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
SQ
Query Match 99.6%; Score 319.8; DB 19; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.7e-91;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
Db 1 gagattgtgctaactcagctccagccaccctgtctctcagccaggagaaaggcgact 60
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Db 61 ctttctgcccagcgccagcaagattattagcaaccacctacactgtgtatcaacaaggcct 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCTGCCAGTCCATCTCTGGATCCCGGCC 180
Db 121 ggtcaagcccaaggcttctcatcmkktatctgccagtcctcatctctggatcccggcc 180
QY 181 AGGTTTCAGTGGCAGTGATGATGAGGAGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240
Db 181 aggttttcagtggcagtgatgagggagacagatttacccctcactatctccagctggagcct 240
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCGAGTGGCCCTCACAGTTCGGAGGG 300
Db 241 gaagattttcagctctattactgtcaacagagtgggcagtggtggcctcacagttcgagggg 300
QY 301 GGGACCAAGGTGGAATAAG 321
Db 301 gggaccaaggtggaaataag 321
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ID V49821 standard; DNA; 321 BP.
XX AC V49821;
XX 02-NOV-1998 (first entry)
XX Vitaxin antibody light chain variable region DNA.
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.
XX Mus sp.

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XX Key Location/Qualifiers
FH 1..321
FT /*tag= a
FT /product= "vitaxin antibody light chain variable region"
FT /note= "partial sequence, no start or stop codon given"
XX WO9833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 38WO-US01826.
XX 30-JAN-1997; 37US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX P-PSDB; W76002.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX Claim 6; Fig 1b; 129pp; English.
XX This sequence encodes the vitaxin antibody variable light chain region.
XX Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX block integrin-mediated signal transduction. This is useful in the
XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
SQ
Query Match 99.3%; Score 318.6; DB 19; Length 321;
Best Local Similarity 99.1%; Pred. No. 4.1e-91;
Matches 318; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
Db 1 gagattgtgctaactcagctccagccaccctgtctctcagccaggagaaaggcgact 60
QY 61 CTTTCTGCCAGCGCAGCAAGTATTAGCACACCTTACACTGTGTATCAACAAGGCGCT 120
Db 61 ctttctgcccagcgccagcaagattattagcaaccacctacactgtgtatcaacaaggcct 120
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Db 121 ggtcaagcccaaggcttctcatcmkktatctgccagtcctcatctctggatcccggcc 180
QY 181 AGGTTTCAGTGGCAGTGATGAGGAGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240
Db 181 aggttttcagtggcagtgatgagggagacagatttacccctcactatctccagctggagcct 240
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCGAGTGGCCCTCACAGTTCGGAGGG 300
Db 241 gaagattttcagctctattactgtcaacagagtgggcagtggtggcctcacagttcgagggg 300
QY 301 GGGACCAAGGTGGAATAAG 321
Db 301 gggaccaaggtggaaataag 321

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RESULT 3
V49823
ID V49823 standard; DNA; 321 BP.
XX AC
XX V49823;
XX DT
XX 02-NOV-1998 (first entry)
XX DE
XX LM609 antibody light chain variable region DNA fragment.
XX KW
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; ss.
XX OS
XX Mus sp.
XX FH
XX Key Location/Qualifiers
XX CDS 1..321
XX FT /*tag= a
XX FT /product= "LM609 antibody light chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"
XX PN
XX W09833919-A2.
XX PD
XX 06-AUG-1998.
XX PF
XX 30-JAN-1998; 98WO-US01826.
XX XX
XX 30-JAN-1997; 97US-0791391.
XX PA
XX (IXSY-) IXSYS INC.
XX PI
XX Glaser SM, Huse WD;
XX XX
XX WPI; 1998-437472/37.
XX DR
XX P-PSDB; W75004.
XX XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX PS
XX Claim 40; Fig 2b; 129pp; English.
XX CC
XX This sequence encodes the LM609 antibody variable light chain region.
XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX block integrin-mediated signal transduction. This is useful in the
XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX SQ
XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 82.8%; Score 265.8; DB 19; Length 321;
Best Local Similarity 88.8%; Pred. No. 1.7e-74;
Matches 285; Conservative 2; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAGATTGCTAAGTCTCCAGCCACCTGCTCTCTCAGCCCGAGGAGAAAGGGGACT 60
DB 1 gatattgtcaactcagctccagccacctgtctgtgacaccagagatagcgtcagt 60
QY 61 CTTTCTCGCCAGCCGAGCAAGTATTAGCAACCCACTACCTGCTATCAACAAGGCT 120
DB 61 ctttctcgccagccagccagcagctattagcaaccacctactactggtatcaacaaataca 120
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 121 catgagtctccaagccttctcatcagtcagtctccagtcagtcagtcagtcagtcagtc 180
QY 181 AGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCACCTCAGTATCTCCAGTCTGGAGCT 240
DB 181 aggttcagtgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 240
QY 241 GAAGATTGTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTCCGAGGG 300
DB 241 gaagatttggaatgtattctgtcaacagatggcagtcggcctcacacagttcggagg 300
QY 301 GGGACCAAGTGGAAATTAAG 321
DB 301 gggaccaagctggaaattaag 321

RESULT 4
235244
ID 235244 standard; cDNA; 381 BP.
XX AC
XX Z35244;
XX DT
XX 13-MAR-2000 (first entry).
XX DE
XX Humanised anti-verotoxin II antibody VTml-1 VL cDNA.
XX KW
XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
XX monoclonal antibody; light chain; mouse; human; humanised antibody;
XX Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
XX HUS; therapy; ss.
XX OS
XX Homo sapiens.
XX XX
XX Synthetic.
XX FH
XX Key Location/Qualifiers
XX FT sig_peptide 1..60 /*tag= a
XX FT mat_peptide 61..381 /*tag= b
XX FT
XX W09959629-A1.
XX PD
XX 25-NOV-1999.
XX PF
XX 19-MAY-1999; 99WO-US11179.
XX PR
XX 20-MAY-1998; 98US-0086570.
XX XX
XX (TEIJ) TEIJIN LTD.
XX PA
XX (PROT-) PROTEIN DESIGN LABS INC.
XX PI
XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX WPI; 2000-086580/07.
XX DR
XX P-PSDB; Y32407.
XX XX
XX Humanized antibody binding to verotoxin II used for treating Verotoxin
XX producing E. coli -
XX PS
XX Disclosure; Fig 2b; 59pp; English.
XX CC
XX This DNA sequence codes for a humanised light chain variable region
XX (see Y32407) of murine monoclonal antibody VTml-1 (MuVTml-1), an
XX antibody that specifically binds to the B subunit of verotoxin II
XX (VT2). The invention relates to humanised antibodies against VT2
XX that are capable of neutralizing VT2 and/or VT2 variants. The
XX humanised antibody is a humanized form of MuVTml-1 comprising the
XX complementarity determining regions of MuVTml-1 (see Y32404-05) and
XX heavy and light chain variable region frameworks from the human GF4
XX antibody heavy and light chain frameworks, provided that at least 1
XX position selected from L49, H29, H30, H49 and H98 is occupied by the
XX amino acid at the equivalent position of the MuVTml-1 antibody heavy
```

CC or light chain variable region framework. Such humanized antibodies
 CC have an affinity for VT2 that is 3-, 5 or 10-times that of MuVtm1-1.
 CC They are used for treating a patient suffering from, or at risk of,
 CC the toxic effects from VT2 (claimed), especially for treating
 CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic
 CC uraemic syndrome (HUS).
 XX
 SQ Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;

Query Match 80.5%; Score 258.4; DB 21; Length 381;
 Best Local Similarity 87.5%; Pred. No. 3.9e-72;
 Matches 280; Conservative 2; Mismatches 38; Indels 0; Gaps 0;
 QY 1 GAGATTGCTCACTCAGTCTCAGCCACCTCTCTCTCAGCCCGGAGGAGGCGACT 60
 Db 61 gaaattgtctaactcagtcctcagccaccctgtctgtctccaggagagagccact 120
 QY 61 CTTTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTTACACTGGTATCAACAAGGCGCT 120
 Db 121 ctttctcgaggccagtcactattagcaaacactacactgtatcaacaagaacca 180
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 Db 181 ggtcaggctccaaggtctctcaagtcgtctccagtcctatctctggatcccgcc 240
 QY 181 AGGTCAGTGGCAGTGCATCAGGACAGATTTCACCTCAGTCTCCAGTCTGGAGGCT 240
 Db 241 aggttcagtgggcagtggtacaggagagatttcactctcactcactcagcagtcgtgaatct 300
 QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTTCGGAGG 300
 Db 301 gaagatttgcagtgattactgtcaacagagattacagtcgctcagtcggtcgtca 360
 QY 301 GGGACCAAGGTGGAATTA 320
 Db 361 gggaccaagtggtgatca 380

RESULT 5
 V71800
 ID V71800 standard; cDNA; 321 BP.
 AC V71800;
 DT 15-MAR-1999 (first entry)
 XX Humanised anti-alpha-v beta-3 MAB D12H2HC 1-0 VL cDNA.
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2HC-10; ds.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9840488-A1.
 PN 17-SEP-1998.
 XX 12-MAR-1998; 98WO-US04987.
 PF 12-MAR-1997; 97US-0039609.
 PR (SMK) SMITHKLINE BEECHAM CORP.
 XX Johanson KO, Jonak ZL, Taylor AH;
 PI WPI; 1999-034590/03.
 XX

P-PSDB; W84098.

XX New anti alpha-v beta-3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

PS Claim 2; Page 61-62; 97pp; English.

XX This DNA sequence codes for the light chain variable region (VL,
 CC see W84098) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
 CC (see W84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions from the murine anti-human
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see
 CC W84094). 3 Murine framework residues (1, 49 and 60) are retained
 CC in the synthetic VL. A humanised VH DNA sequence is also provided
 CC (see W71799). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor; e.g. cardiovascular disorders or angioenic-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.

XX Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 other;

Query Match 78.0%; Score 250.4; DB 20; Length 321;
 Best Local Similarity 85.9%; Pred. No. 1.2e-69;
 Matches 275; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCGGAGGAGGCGACT 60
 Db 1 gacatagctactgactcagtcctccagccctgtcttctccaggagagagccacc 60
 QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACCACTACACTGTGTATCAACAAGGCGCT 120
 Db 61 ctttctcgaggccagccaaagtattagcaaccactacactggtatcaacaacaaact 120
 QY 121 GGTCAAGCCCGCAGGCTTCATCMKKATATCGTTCGCCAGTCCATCTCTGGATCCCGGCC 180
 Db 121 ggcacggctcgcggcttctcatcaagtgtctccagtcctctctggatccctcc 180
 QY 181 AGGTTCACTGTCAGTGGATCAGGACAGATTTCACCTCAGTCTCAGTCTGGAGCT 240
 Db 181 aggttcagtgcaatgagtcagggacagagatttcaactcaccatcagcgtctagagcct 240
 QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCACACGTTTCGGAGG 300
 Db 241 gaagatttgcggtttattactgtcaacagagtaacagtcggcctttcaagtcggcag 300
 QY 301 GGGACCAAGGTGGAATTA 320
 Db 301 ggtaccaagtggaataaa 320

RESULT 6

V71802

ID V71802 standard; cDNA; 338 BP.

XX V71802;

XX 15-MAR-1999 (first entry)

XX Vitronectin alpha-v beta-3 MAB VL cDNA.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCTCCAGTCATCTCTGGATCCCGCC 180
 Db 181 catgagttctcaaggcttctcaagtaagtcttccagtcacatctctgggataccctcc 240
 QY 181 AGGTTCAAGGCGAGTGATCAGGACAGATTCACCTCAGTCATCTCCAGTCGGAGCCT 240
 Db 241 aggttcagtgagtgagtcagggacagatttcactctcagtcacacagtgaggagact 300
 QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCCTCACACGTTCCGAGG 300
 Db 301 gaagattttggaatgatttctctcaacagagtaacagtgagctgagctgagctgagct 360
 QY 301 GGGACCAAGGTGGAAATTA 320
 Db 361 gggaccaagctggagctgaa 380

RESULT 8
 ID Q04654 standard; DNA; 5238 BP.
 AC Q04654;
 XX
 DT 01-OCT-1990 (first entry)
 DE Plasmid pBR111 encoding antibody MAK33 kappa chain.
 KW Antibody MAK33; kappa chain; plasmid pBR111; activated antibody; ss.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..663
 FT /*tag= a
 FT /product= kappa chain of MAK33
 XX
 PN DE3835350-A.
 XX
 PD 19-MAR-1990.
 PF 17-OCT-1988; 88DE-3835350.
 XX
 PR 17-OCT-1988; 88DE-3835350.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Rudolph R, Buchner J, Lenz H;
 XX
 DR WPI; 1990-156813/21.
 XX
 PT Activated antibody prodn. from recombinant prokaryotic cells -
 PT by solubilisation under reducing conditions, then oxidative
 PT renaturation, carried out at low protein concn.
 XX
 PS Disclosure; ; p; German.
 XX
 CC Plasmid pBR111 encoding the kappa chain and plasmid p10169 encoding
 CC the fd chain of antibody MAK33 were used to transform E.coli DSM 3689 and
 CC the resulting cells grown to form inclusion bodies. After the final
 CC renaturation step an 18% yield of biologically-active protein was
 CC produced.
 CC see also Q04655.
 XX
 SQ Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;

Query Match 74.6%; Score 239.6; DB 11; Length 5238;
 Best Local Similarity 84.1%; Pred. No. 8.3e-66;
 Matches 269; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 1 GAGATTGTCTAACTCAGTCTCCAGCCACCTGCTCTCTCAGCCGAGGAGGAGGCGACT 60
 Db 7 gatattgtctaaactcagtcctccagccaccctgtctgtgactcccaagagatagcgtcagt 66
 QY 61 CTTTCTGCGCCAGCCAGCCAAAGTATTAGCAACCACTTACACTGGTATCAACAAGGCGCT 120

Db 67 ctctctcagggccagccaaagtattagcaaacctacactggtatcaacaaaatca 126
 QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCTCCAGTCATCTCTGGATCCCGCC 180
 Db 127 catgagttctcaaggcttctcattcaataatctctccagtcacatctctgggataccctct 186
 QY 181 AGGTTCAAGGCGAGTGATCAGGACAGATTCACCTCAGTCATCTCCAGTCGGAGCCT 240
 Db 187 aggttcagtgagtgagtcagggacagatttcactctcagtcacacagtgaggagact 246
 QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCCTCACACGTTCCGAGG 300
 Db 247 gaagattttggaatgatttctctcaacagagtaacagtgagctgagctgagctgagct 306
 QY 301 GGGACCAAGGTGGAAATTA 320
 Db 307 gggaccaagctggagctgaa 326

RESULT 9
 V71798
 ID V71798 standard; cDNA; 324 BP.
 AC V71798;
 XX
 DT 15-MAR-1999 (first entry)
 DE Murine vitronectin alpha-v beta-3 receptor MAB VL CDNA.
 XX
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
 XX
 OS Mus sp.
 XX
 PN WO9840488-A1.
 XX
 PD 17-SEP-1998.
 XX
 PF 12-MAR-1998; 98WO-US04987.
 XX
 PR 12-MAR-1997; 97US-0039609.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Johanson KO, Jonak ZL, Taylor AH;
 XX
 DR WPI; 1999-034590/03.
 DR P-FSDB; W84094.
 XX
 PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Example 13; Page 59-60; 97pp; English.
 XX
 CC This cDNA sequence codes for the light chain variable region (VL,
 CC see W84094) of the anti-human alpha-v beta-3 vitronectin receptor
 CC murine monoclonal antibody D12. It was obtained from hybridoma
 CC total RNA by RT-PCR using mouse kappa and N-terminal-based primers
 CC (see V71808-09). A heavy chain variable region clone (see V71797)
 CC has also been identified. D12 VH and VL show sequence similarity
 CC to Kabat VH subgroup I (see W84095) and Kabat VK subgroup III (see
 CC W84096), respectively. Humanised VH (see W84097) and VL (see
 CC W84098) were constructed by combining the framework regions of the
 CC human V region consensus sequences with complementarity determining
 CC regions of D12 (keeping some preferred murine framework residues).
 CC The humanised antibodies are specifically reactive with the human

CC alpha-v beta-3 protein receptor and capable of neutralising the
CC receptor. They can be used for passive immunotherapy of a disorder
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC disorders or angiogenic-related disorders, such as angiogenesis
CC associated with diabetic retinopathy, atherosclerosis and
CC restenosis, chronic inflammatory disorders, macular degeneration,
CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC diseases where bone resorption is associated with pathology such as
CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
CC of malignancy, osteolytic lesions produced by bone metastasis, bone
CC loss due to immobilisation or sex hormone deficiency. They can also
CC be used for targeted drug therapy, and for detection and diagnosis.
XX
SQ Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;

Query Match 74.5%; Score 239.2; DB 20; Length 324;
Best Local Similarity 83.8%; Pred. No. 4e-66; Indels 0; Gaps 0;
Matches 268; Conservative 2; Mismatches 50;
QY 1 GAGATTGTGCTAAGTCTCCAGCCACCTGCTCTCTCAGCCCGAGGAGGCGGACT 60
DB 1 gacattgtgactcagctcagccaccctgtctgtgactccagagatagcgtcagt 60
QY 61 CTTTCTGCCAGCGCCAGCAAGTATTAGCACCCCTACACTGTGTATCAACAAGGCGCT 120
DB 61 ctttctgcaggccagccaaagtattagcaaccactacactggtatcaacaagatca 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCAGTCCATCTCGGATCCCGCC 180
DB 121 catgagctcccaaggcttctcatcagtagtcttccagctcatctctggatccctcc 180
QY 181 AGGTTTCAGTGGAGTGGATCGAGGACAGATTTCACCTCATCTCTCCAGTCTGGAGCGCT 240
DB 181 aggttcagagcagtgatcgacagggacagatttcactctcaatcaatcatttggagact 240
QY 241 GAAGATTTGTCAGTCTATTACTGTCAACAGAGTGGCGAGTGGCCCTCACAGTTCGGAGGG 300
DB 241 gaggattttggatgtattctgtcaacagagtaacagctggccttcacgttcgctcg 300
QY 301 GGGACCAAGTGGAAATTA 320
DB 301 gggacaacttggaaataa 320

RESULT 10
235242
ID 235242 standard; cDNA; 381 BP.
XX
AC 235242;
XX
DT 13-MAR-2000 (first entry)
XX
DE Mouse anti-verotoxin II antibody VTml-1 VL cDNA.
XX
KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
KW monoclonal antibody; light chain; mouse; humanised antibody;
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW HUS; therapy; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /tag= a
FT mat_peptide 58..381
FT /tag= b
FT /transl_except= (pos:184..186, aa:lys)
XX
PN W09959629-A1.
XX
PD 25-NOV-1999.
XX

PF 19-MAY-1999; 99WO-US11179.
PR 20-MAY-1998; 98US-0086570.
XX (TEIJ) TEIJIN LTD.
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX WPI; 2000-086580/07.
DR P-PSDB; Y32405.
XX
PT Humanized antibody binding to verotoxin II used for treating Verotoxin
PT producing E. coli -
XX
PS Disclosure; Fig 1b; 59pp; English.
XX
CC This DNA sequence codes for the light chain variable region (see
CC Y32405) of murine monoclonal antibody VTml-1 (MuVTml-1), an
CC antibody that specifically binds to the B subunit of verotoxin II
CC (VT2). The invention relates to humanised antibodies against VT2
CC that are capable of neutralizing VT2 and/or VT2 variants. The
CC humanised antibody is a humanized form of MuVTml-1 comprising the
CC complementarity determining regions of MuVTml-1 and heavy and
CC light chain variable region frameworks from the human GF4 antibody
CC heavy and light chain frameworks, provided that at least 1 position
CC selected from L49, H29, H30, H49 and H98 is occupied by the amino
CC acid at the equivalent position of the MuVTml-1 antibody heavy or
CC light chain variable region framework. Such humanized antibodies
CC (see Y32406-07) have an affinity for VT2 that is 3-, 5 or 10-times
CC that of MuVTml-1. They are used for treating a patient suffering
CC from, or at risk of, the toxic effects from VT2 (claimed), especially
CC for treating verotoxin producing Escherichia coli (VTEC) infection,
CC and haemolytic uraemic syndrome (HUS).
XX
SQ Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;

Query Match 72.5%; Score 232.8; DB 21; Length 381;
Best Local Similarity 82.5%; Pred. No. 4.4e-64;
Matches 264; Conservative 2; Mismatches 54; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAAGTCTCCAGCCACCTGCTCTCTCAGCCCGAGGAGGCGGACT 60
DB 61 gatgtgtgctaaactcagctcagccaccctgtctgtgactccagagatagcgtcagt 120
QY 61 CTTTCTGCCAGCGCCAGCAAGTATTAGCACCCCTACACTGTGTATCAACAAGGCGCT 120
DB 121 ctttctgcaggccagctcagctcagccaccctgtctgtgactccagagatagcgtcagt 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCAGTCCATCTCGGATCCCGCC 180
DB 181 catgagctcccaaggcttctcatcagtagtcttccagctcatctctggatccctcc 240
QY 181 AGGTTTCAGTGGAGTGGATCGAGGACAGATTTCACCTCATCTCTCAGTCTGGAGCGCT 240
DB 241 aggttcagtgagcagtgatcgacagggacagatttcactctcagtagtcaacagtggaact 300
QY 241 GAAGATTTGTCAGTCTATTACTGTCAACAGAGTGGCGAGTGGCCCTCACAGTTCGGAGGG 300
DB 301 gaggattttggatgtattctgtcaacagagttacagctggcgcgtcactcttgggtgct 360
QY 301 GGGACCAAGTGGAAATTA 320
DB 361 gggacccaagctggagactgaa 380
XX
RESULT 11
T49345
ID T49345 standard; cDNA; 416 BP.
XX
AC T49345;
XX

Query Match	71.5%	Score	229.6	DB	18	Length	416
Best Local Similarity	81.9%	Pred. No.	4.6e-63				
Matches	262	Conservative	2	Mismatches	56	Indels	0
Gaps							
QY	1	GAGATTGTCTAACTCAGTCTCCAGCCACCCCTGCTCTCAGCCCGAGGAAAGGGCGACT	60				
Db	76	gaatogtactgactcagtcctcagccacgctgtctttagtccaggagaaagagccacc	135				
QY	61	CTTCTCTGCCAGGCGCCAAAGATTATAGCAACACCTACTGTGTATCAACAAAGGCT	120				
Db	136	ctctctcgaggccagtcagagtattggcacaatacactggtatcagcaagacct	195				
QY	121	GGTCAGCCCCAAGGCTTCTATCMKKTATCGTTCACAGTCCCATCTCTGGGATCCCCGGC	180				
Db	196	ggccaggctccaggctctccataaagtagtgccttgtagtctatctctggaatccctgpc	255				
QY	181	AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACCCCTCAGTATCTCCAGCTGTGAGCGT	240				
Db	256	aggttttagtgagtgagtcaggggacagattttactcttaccatcagcagctgtagcct	315				
QY	241	GAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGGCTCACACGTTTCGGAGGG	300				
Db	316	gaagattttgagtttattactgtcaacaaaaataataactggccaaaccagcttcggtgga	375				

Query Match	71.0%	Score 228;	DB 17;	Length 324;
Best Local Similarity	81.6%;	Pred. No. 1.3e-52;		
Matches 261;	Conservative	2;	Mismatches 57;	Indels 0;
Gaps	0;			

QY	1	GAGATTGTTCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT	60
Db	1	gacatccagctgacccagttccagccaccctgtctgtgactccaggagatagcgtcagct	60
QY	61	CTTTCTCGCCAGGCCAGCAAGTATTAGCAACCACCTACACTGGTGTATCAACAAGGCCT	120

Db 61 cttctctagggcagcaagattagcaacagcctacactggtatcaacaaataca 120
 Qy 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCAGTCCATCTCTGGGATCCCGCC 180
 Db 121 catgagtccaagcctctcatcaagatgtttccagtcctctctggtatccctcc 180
 Qy 181 AGGTTCACTGGCAGTGATCAGGACAGATTCACCCCTACATCTCCAGTCTGGAGCCT 240
 Db 181 aggttcagggcagtgagatcagggacagatttcactctcactatcaacagtgaggagat 240
 Qy 241 GAAGATTTGCACTATTACTGTCAACAGAGTGCAGCTGCCCTCACACGTTCCGAGGG 300
 Db 241 aaagatttggaaatgtattctgtcaacagagtgacagtggtgagcgttcggtgga 300
 Qy 301 GGGACCAAGGTGGAATTA 320
 Db 301 gggaccaagctggagatcaa 320

RESULT 13

Q43245

ID Q43245 standard; DNA; 486 BP.

XX AC Q43245;

XX DT 13-OCT-1993 (first entry)

XX DE hIL2R Ab L chain V region DNA.

XX KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;

XX KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;

XX KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;

XX KW region; PCR; framework; plasmid; heavy; H; light; L; ss.

XX OS Mus musculus/Homo sapiens.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 136..455

XX FT /*tag= a

XX PN WO9311238-A.

XX PD 10-JUN-1993.

XX PF 03-DEC-1992; 92WO-JP01583.

XX PR 06-DEC-1991; 91JP-0323319.

XX PA (BIOT) BIOTEST PHARMA GMBH.

XX PA (INNO-) INNOTHERAPIE LAB.

XX PA (SUNU) SUMITOMO PHARM CO LTD.

XX PI Gomi H, Nakatani T, Noguchi H, Wajdenes J;

XX DR WPI; 1993-197057/24.

XX DR P-PSDB; R37612.

XX PT Humanised antibody comprising - CDR region of mouse MAB B-B10

XX PT specific for IL-2 receptor useful for treating carcinoma

XX PT expressing IL-2 receptor

XX PS Disclosure; Fig 5; 62pp; English.

XX CC The sequences given in Q43244-45 encode the heavy (H) and light (L)

XX CC chain variable (V) regions of a humanised antibody (Ab) which binds

XX CC specifically to human interleukin (IL)-2 receptor (hIL2R). The

XX CC complementarity-determining regions (CDRs) of these V regions were

XX CC derived from the murine anti-human IL-2 receptor monoclonal Ab (Mab)

XX CC B-B10 (see also R37599-04). This Mab is antagonistic to the binding

XX CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits

XX CC the human mixed lymphocyte reaction. The cDNA encoding the variable

XX CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also

CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.
 XX SQ Sequence 486 BP; 136 A; 109 C; 110 G; 131 T; 0 other;

Query Match 69.7%; Score 223.6; DB 14; Length 486;

Best Local Similarity 80.9%; Pred. No. 3.8e-61;

Matches 259; Conservative 1; Mismatches 60; Indels 0; Gaps 0;

Qy 1 GAGATTGCTGAACCTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
 Db 136 gagatcgctcgtactcagctccaggcacactgtctctgagtcaggagaaagagccaca 195
 Qy 61 CTTTCTGCCAGGCGCCAAAGTATTAGCAACCACTACACTGATGATCAACAAGGCGCT 120
 Db 196 ctgtcctcagggccagtcagaccattggcacaagcatcacactggtatccagcagagacca 255
 Qy 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCCAAGTCCATCTCTGGATCCCGCC 180
 Db 256 ggcagggcccaaggctctctcatatattctgtctgtatctctctggtatccagcagagacca 315
 Qy 181 AGGTTCACTGGCAGTGATCAGGACAGATTCACCCCTACATCTCCAGTCTGGAGCCT 240
 Db 316 aggttagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 375
 Qy 241 GAAGATTTGCACTATTACTGTCAACAGAGTGCAGCTGCCCTCACACGTTCCGAGGG 300
 Db 376 gaagatttcgagctctattactgtcaacaagtagtagtggtggtggtggtggtggtggt 435
 Qy 301 GGGACCAAGGTGGAATTA 320
 Db 436 gggaccaaggtcgagatcaa 455

RESULT 14

Z10202

ID Z10202 standard; DNA; 8858 BP.

XX AC Z10202;

XX DT 01-NOV-1999 (first entry)

XX DE Expression vector of light chain of chimeric anti-CD40 antibody chi22.

XX KW Light chain variable region; chimeric antibody; anti-CD40 antibody;

XX KW chi220; humoral immune response; T cell dependent antigen;

XX KW collagen induced arthritis; transplant induced rejection;

XX KW T cell mediated disorder; autoimmune disease; inflammatory disease;

XX KW transplantation; ss.

XX OS Synthetic.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 1065..1388

XX FT /*tag= a

XX FT /note= "no termination sequence"

XX PN WO9942073-A2.

XX PD 26-AUG-1999.

XX PF 10-FEB-1999; 99WO-US02949.

XX PR 19-FEB-1998; 98US-0026291.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;

PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;
XX WPI; 1999-527408/44.
XX Antibody that binds human CD40, for treating T cell mediated
PT disorders
XX
PS Claim 18; Fig 14A-C; 77pp; English.
XX
CC The present sequence represents an expression vector for expressing
CC the light chain of a chimeric anti-CD40 antibody designated ch220.
CC The antibodies are effective in modulating humoral immune response
CC against T cell dependent antigens, collagen induced arthritis and
CC transplant induced rejection. They are also useful for their
CC anti-inflammatory properties. The antibodies have wide therapeutic
CC applications, including autoimmune and inflammatory diseases and
CC transplantation. The antibody can be used in a pharmaceutical composition
CC for treating a patient suffering from a T cell mediated disorder. They
CC can also be used to treat autoimmune diseases, inflammatory diseases,
CC and transplantation.
XX
SQ Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;

Query Match 69.7%; Score 223.6; DB 20; Length 8858;
Best Local Similarity 80.9%; Pred. NO. 1.1e-60;
Matches 259; Conservative 1; Mismatches 60; Indels 0; Gaps 0;
QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGCGACT 60
DB 1065 gacattgtctgactcagctccagccacctgtgtgactccaggagatagagtctct 1124
QY 61 CTTTCTCTGCGAGGCGAGCAAGTATTAGCAACCACTACACTGTATCAACAAGGCGCT 120
DB 1125 cttcttcagggccagcagagattagcagactactactactggtatcaacaataca 1184
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCCGCC 180
DB 1185 catgagttccaaaggcttctcatcaaatgtcttcccttccatctctggtatccctcc 1244
QY 181 AGGTTCACTGGCAGTGGATCAGGGACATTTACCTACCTACTATCTCAGTCTGGAGGCT 240
DB 1245 aggttcagtgagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1304
QY 241 GAAGATTGTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTTCACACAGTTCGGAGG 300
DB 1305 gaagatgttggaattattactgtcaacatggtcagagcttccgtgagcgttcgggtgga 1364

RESULT 15
T38510
ID T38510 standard; DNA; 363 BP.
XX
AC T38510;
XX
DT 23-JUN-1997 (first entry)
XX
DE Light chain coding sequence of monoclonal antibody 4B4-1-1.
XX
KW Antibody; human; heavy chain; variable region; light chain; Mab; 4-1B8;
KW tumour necrosis factor receptor; membrane protein; accessory molecule;
KW T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;
KW immunosuppressive agent; autoimmune disease; rejection response; therapy;
KW organ transplantation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..324

FT /*tag= a
FT /note= "claimed light chain variable region coding
FT sequence"
FT 325..363
FT /*tag= b
FT /note= "constant region (encoded protein not given in
FT specification)"
XX
XX PN WO9632495-A1.
XX
XX PD 17-OCT-1996.
XX
XX PF 06-APR-1996; 36WO-KR00045.
XX
XX PR 08-APR-1995; 35KR-0008176.
XX
XX PA (GLDS) LG CHEM LTD.
XX
XX PI Kang CY, Kim JG;
XX
XX DR WPI; 1996-477145/47.
XX
XX DR P-PSDB; W04333.
XX
XX PS Claim 4; Fig 3a; 37pp; English.
XX
CC T38509 and T38510 represent the coding sequences for the variable regions
CC of the heavy and light chains of the antibody of the invention. This
CC sequence is stated in the specification as being 372 bp in length, but
CC only comprises 363 bp. The antibody of the invention (designated 4B4-1-1)
CC is a monoclonal antibody (Mab) specific for human 4-1BB. 4-1BB encodes a
CC member of the tumour necrosis factor receptor family of integral membrane
CC proteins. 4-1BB is an accessory molecule expressed on the surface of
CC T-cells in the initial stage of activation. The accessory molecules on
CC the T-cell bind to the corresponding ligand on the antigen-presenting
CC cell and this accelerates the activation of the T- and antigen-presenting
CC cells, thereby promoting various immune responses. The Mab is specific
CC for human 4-1BB, which is selectively expressed on activated T-cells. The
CC Mab is useful as an immunosuppressive agent. It can be used for the
CC treatment of autoimmune diseases, such as rheumatoid arthritis, and for
CC preventing rejection response after organ transplantation.
XX
SQ Sequence 363 BP; 91 A; 102 C; 79 G; 91 T; 0 other;

Query Match 69.2%; Score 222; DB 17; Length 363;
Best Local Similarity 80.6%; Pred. NO. 1.1e-60;
Matches 258; Conservative 1; Mismatches 61; Indels 0; Gaps 0;
QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGCGACT 60
DB 1 gacattgtgagtcagcagctccagccacctgtgtgactccaggagatagagtctct 60
QY 61 CTTTCTCTGCGAGGCGAGCAAGTATTAGCAACCACTACACTGTATCAACAAGGCGCT 120
DB 61 cttcttcagggccagcagagattagcagactactactactggtatcaacaataca 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCCGCC 180
DB 121 catgagttccaaaggcttctcatcaaatgtcttcccttccatctctggtatccctcc 180
QY 181 AGGTTCACTGGCAGTGGATCAGGGACATTTACCTACCTACTATCTCAGTCTGGAGGCT 240
DB 181 aggttcagtgagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
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DB 241 gaagatgttgagtgatattactgtcaacatggtcagagcttccctccagcgttcgggtgga 300
QY 301 GGGACCAAGTGGGAATTAA 320

Db 301 ggcaccaagctggaatcaa 320
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Search completed: February 25, 2001, 09:56:42
Job time: 5577 sec

W/016 JF7701000000

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 09:14:29 ; Search time 75.17 seconds
(without alignments)
688.206 Million cell updates/sec

Title: US-08-790-540A-3
Perfect score: 321
Sequence: 1 GAGATTGTGCTAACTAGTC.....GGACCAAGTGGGAATTAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues
Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	245.6	76.5	381	1	US-08-477-728-82
3	245.6	76.5	381	1	US-08-474-040-82
4	245.6	76.5	381	1	US-08-487-200-82
5	245.6	76.5	424	1	US-08-436-463-3
6	239.6	74.6	5238	5	5453363-1
7	224.8	70.0	321	2	US-08-232-081B-35
8	223.6	69.7	321	2	US-08-232-081B-36
9	222	69.2	324	2	US-08-737-560A-13
10	222	69.2	363	2	US-08-737-560A-8
11	213.6	66.5	322	2	US-08-476-176B-3
12	213.6	66.5	322	3	US-08-127-721A-3
13	213.6	66.5	322	3	US-08-485-246A-3
14	204	63.6	321	2	US-08-232-081B-39
15	201	62.6	318	1	US-08-326-362-3
16	198.8	61.9	318	2	US-08-800-198-3
17	198.8	61.9	318	3	US-09-296-595-3
18	198.8	61.9	720	3	US-08-800-198-7
19	198.8	61.9	720	3	US-09-296-595-7
20	198	61.7	720	2	US-07-956-399-1
21	193.8	60.4	429	2	US-08-653-402B-7
22	191.2	59.6	321	1	US-08-192-102-2
23	191.2	59.6	321	1	US-08-324-799-2
24	191.2	59.6	321	2	US-08-192-861A-2
25	191.2	59.6	717	2	US-07-956-399-3
26	187.2	58.3	812	1	US-08-053-131-178
27	187.2	58.3	812	1	US-08-096-762-178
28	180.8	56.3	900	1	US-08-053-131-180

29	180.8	56.3	900	1	US-08-096-762-180
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35	172	53.6	424	2	US-08-476-176B-9
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37	172	53.6	424	3	US-08-485-246A-9
38	170.8	53.2	321	3	US-08-783-853A-43
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41	170.4	53.1	424	3	US-08-485-246A-7
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ALIGNMENTS

RESULT 1
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Sequence 180, Appl
Sequence 19, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 43, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 3, Appl

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: COELINGH, Kathleen F.
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-474-040-82

Query Match 76.5%; Score 245.6; DB 1; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGTCCGGGATAGCGTCACT 120
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCTCC 240
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DB 241 AGGTTCAAGGAGTGGATCAGGACAGATTTACCCCTCATCTCTCACTCTGGAGCT 300
QY 241 GAAGATTTGCACTTATTACTGTCAACAGAGTGGGAGTGGGCTTCAACAGGCT 300
DB 301 GAAGATTTGCACTTATTACTGTCAACAGAGTGGGAGTGGGCTTCAACAGGCT 360
QY 301 GGGACCAAGTGGAAATTA 320
DB 361 GGGACCAAGTGGAAATTA 380

RESULT 4
US-08-487-200-82
Sequence 82, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
ATTORNEY: CO, Man Sung

APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-487-200-82

Query Match 76.5%; Score 245.6; DB 1; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGTCCGGGATAGCGTCACT 120
QY 61 CTTTCTGCGAGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120
DB 121 CTTTCTGCGAGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCTCC 240
QY 181 AGGTTCAAGGAGTGGATCAGGACAGATTTACCCCTCATCTCTCACTCTGGAGCT 240
DB 241 AGGTTCAAGGAGTGGATCAGGACAGATTTACCCCTCATCTCTCACTCTGGAGCT 300

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Query Match      69.2%; Score 222; DB 2; Length 363;
Best Local Similarity 80.6%; Pred. No. 2e-62;
Matches 259; Conservative 1; Mismatches 61; Indels 0; Gaps 0;
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Q _Y	61	CTTATCTGGCCAGGCGACGCAAGATATATAGAACACCTATACATGCTGTCAACAAGCCCT	120
D _b	61	CTTCTCTCGACGGGCGACGCGACACTATTATAGGCACTATTACCTGGTATATCAACAAAATCA	120
Q _Y	121	GGTCAGAGCCCCAGAGCTTCTCATCMKRTATCGTTCCGACATCTCTGGGATCCCGCC	180
D _b	121	CATGAGTCTCCCAAGGCTTCTCATCAAAATATGCTTCCCAATTCATCTCTGGGATCCCGTCC	180
Q _Y	181	AGGTTTCAGTGGCAGTGGATCGATCGGACAGATTTTACCCCTACTATCTCCAATCTGGAGCCT	240
D _b	181	AGGTTTCAGTGGCAGTGGATCGATCGGAGATTTTACCTCTCATATCAACAAGTGGAACTT	240
Q _Y	241	GAAAGTTTTGCACTATATTACTGTCACAGAGTGGACATGGCCCTACAGCTTCGAGGG	300
D _b	241	GAAAGTGTGGAGTGTATTACTGTCACAGATGGTCAACAGCTTCTCTCGAGATTCGGGGA	300
Q _Y	301	GGGACCAAGTGGAAATTA 320	
D _b	301	GGACCAAGTGGAAATCA 320	

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
OTHER INFORMATION: /product= "light chain variable"
OTHER INFORMATION: domain of murine antibody TBS-C21"
US-08-127-721A-3

Query Match 66.5%; Score 213.6; DB 3; Length 322;
Best Local Similarity 78.8%; Pred. No. 9.3e-60;
Matches 252; Conservative 2; Mismatches 66; Indels 0; Gaps 0;

QY 1 GAGATTGCTACTACAGCTCCAGCCACCTGTCTCTCAGCCGAGGAGGAGGAGCT 60
DB 1 GACATCTTCTCTCAGCTCAGCTCCAGCCATCTGTCTGTAGTCAGGAGGAGGAGCT 60
QY 61 CTTTCTGCGCAGGCGCAGCCAAAGTATTAGCAACCACTACCTGTATCAACAAAGGCT 120
DB 61 TTCTCTGAGGCGCAGCTAGAGCATGTGCAACAACATACCTGTATCAGCAAGAGT 120
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QY 181 AGGTCAGTGGAGTGGATCAGGAGCATTTACCCCTCATCTCCAGCTGTGAGGCT 240
DB 181 AGGTTAGTGGAGTGGATCAGGAGCATTTACTCTTAACATCAGCTGTGAGGCT 240
QY 241 GAGATTTTGCAGTCTATCTATCTGCAACAGAGTGGCAGCTGCTCAGCTTGGAGGG 300
DB 241 GAGATTTTGCAGTCTATCTATCTGCAACAGAGTGGCAGCTGCTGAGGCT 300
QY 301 GGGACCAAGGTGGAATTA 320
DB 301 GGGACCAAGCTGAGATTA 320

RESULT 13

US-08-485-246A-3
Sequence 3, Application US/08485246A
Patent No. 6072035

GENERAL INFORMATION:

APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against a
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6072035artis Patent Department
STREET: 59 Route 10.
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992

ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
OTHER INFORMATION: /product= "light chain variable"
OTHER INFORMATION: domain of murine antibody TBS-C21"
US-08-485-246A-3

Query Match 66.5%; Score 213.6; DB 3; Length 322;
Best Local Similarity 78.8%; Pred. No. 9.3e-60;
Matches 252; Conservative 2; Mismatches 66; Indels 0; Gaps 0;

QY 1 GAGATTGCTACTACAGCTCCAGCCACCTGTCTCTCAGCCGAGGAGGAGGAGCT 60
DB 1 GACATCTTCTCTCAGCTCAGCTCCAGCCATCTGTCTGTAGTCAGGAGGAGGAGCT 60
QY 61 CTTTCTGCGCAGGCGCAGCCAAAGTATTAGCAACCACTACCTGTATCAACAAAGGCT 120
DB 61 TTCTCTGAGGCGCAGCTAGAGCATGTGCAACAACATACCTGTATCAGCAAGAGT 120
QY 121 GGTCAAGCCCCAGGCTTCTCATCMKKTATGCTTCCAGCTCATCTCTGGATCCCCGCC 180
DB 121 GATGCTTCTCCAGGCTTCTCATMAAGTATGCTTGTGATCTATCTCTGGATCCCCGCC 180
QY 181 AGGTCAGTGGAGTGGATCAGGAGCATTTACCCCTCATCTCCAGCTGTGAGGCT 240
DB 181 AGGTTAGTGGAGTGGATCAGGAGCATTTACTCTTAACATCAGCTGTGAGGCT 240
QY 241 GAGATTTTGCAGTCTATCTATCTGCAACAGAGTGGCAGCTGCTCAGCTTGGAGGG 300
DB 241 GAGATTTTGCAGTCTATCTATCTGCAACAGAGTGGCAGCTGCTGAGGCT 300
QY 301 GGGACCAAGGTGGAATTA 320
DB 301 GGGACCAAGCTGAGATTA 320

RESULT 14

US-08-232-081B-39
Sequence 39, Application US/08232081B
Patent No. 5686152

GENERAL INFORMATION:

APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: 150 BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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* SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
US-08-232-081B-39

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Query Match	63.6%;	Score 204;	DB 2;	Length 321;
Best Local Similarity	76.9%;	Pred. No. 1.1e-56;		
Matches 246; Conservative	2;	Mismatches 72;	Indels 0;	Gaps 0

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Db	1	GACATCTTGGCTAGACTCAGTCTCCAGCATCTCTGTGATGCCAGGAAAGAGTCACT	60
QY	61	CTTTCCTGCCAGGCCAGCCAAAGTATTAGCACACCCTAACACTGTTCTCAACAAGGCT	120
Db	61	TTCTCTGCAAGGGCCAGTCAAGACCATTGGGCAAGAAGTAACTAGTCTACGCGAAGACA	120
QY	121	GGTAAACCCCAAGGCTTCTCATCMKRTATGCTCCAGTCACTATCTGTGGATCCCGCC	180
Db	121	AATGGTTCTCCAAAGCTTCTCATTAAGTATGCTTCTGAGTCTATCTCTGGGATCCCTCC	180
QY	181	AGGTTCACTGAGTGGATGATCAGGAGACAGATTTCAACCTCACTATCTTCCAGTTGGAGCT	240
Db	181	AGGTTTATGTGGCACTGGATCAGGGACAGATTTTACTTTAGCATCAACAGCTGTGGAGTCT	240
QY	241	GAAATTTTGGAGTCTATTAATGTCACAAGAGTGGCAGTGGCCTCAGACGTTGGAGG	300
Db	241	GAAATATTTGGAGTTTATTAATGTCACAACAAGTATGATGCTGGCCGCTCAGAGTTGGGCT	300
QY	301	GGGACCAAGCTGGCAATTTAA 320	
Db	301	GGGACCAAGCTGGAGCTGAA 320	

RESULT 15
US-08-326-362-3
Sequence 3, Application US/08326362
Patent No. 5730981
GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESS: Finnegan, Henderson, Farab
ADDRESS: Finnegan, Henderson, Farab
ADDRESS: Finnegan, Henderson, Farab
STREET : 1300 I Street, N.W., Suite 700
CITY : Washington
STATE : D.C.
COUNTRY : USA
ZIP : 20005-3315

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Review #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,362
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795.3
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elnauck, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1276-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-326-362-3

```

Query Match	:	62.68;	Score 201;	DB 1;	Length 318;
Best Local Similarity	:	76.78;	Pred. No. 1e-55;		
Matches 243;	Conservative	2;	Mismatches	72;	Indels 0;
			Gaps		0;

OY	1	GAGATTGGCAATCACTAGTCTCCAGGCCACTGTCTCTCAGGCCAGGAGAAAGGGCACT	60
Db	1	GACATCCAGTCAGACCCAGTCTCCAGCCATCTGTCTGTAGTCCAGSAGAAAGAGTAACT	60
OY	61	CTTTCCTGCGCCAGGCCAGCCAAAGTATTAGCAACCACCTACACTGTGTATCAACAAAGGCT	120
Db	61	TTCCCTTCGCTGGGCCACATCAGAGCATTTGGGACACAGCATATACACTGGTATATCAACAAAGAAC	120
OY	121	GGTAAAGCCCAAGGCTTCTCATCMKATTAATGTTCCAGTCCATCTCTGGGATCCCGCC	180
Db	121	AATGGTCTCTCCAAAGCTCTTCTCATTAATATTTCTCTTGAAGTCTATCTCTGGGATCCCTCC	180
OY	181	AGGTTCACTGGCAGTGGATGATCAGGACAGATTTTCAACCTCACTATCTTCCAGTCTGGAGCCT	240
Db	181	AGGTTTATGTGGCAATGGATATAGGGACAGATTTTAACTTTGACATCAACAAGATTTGGAACTCT	240
OY	241	GAAATATTTGGAGTCTATTACTGTCAACAGAGTGGAGTGGCTCAGAGTTGCGAGGG	300
Db	241	GAAATATTTGGAGTATTATTACTGTCAACAAACTATATAGTGGGCATTTCAAGTTTGGCTCG	300
OY	301	GGGACCAAGGTGGAAAT	317
Db	301	GGGACCAAGGTGGAGAT	317

Search completed: February 25, 2001, 09:14:34
Job time: 15049, sec.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:04:13 ; Search time 23.47 Seconds
(without alignments)
309.560 Million cell updates/sec

Title: US-08-790-540a-4

Perfect score: 557
Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSPHPTFGGGRVKEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	84.4	144	2	PI0106
2	460	82.6	111	2	S23628
3	458	82.2	128	2	A56701
4	457	82.0	128	2	S40379
5	452.5	81.2	114	2	S54905
6	451	81.0	108	2	G44151
7	447	80.3	106	2	PC4282
8	447	80.3	107	2	B45722
9	444	79.7	117	2	S40362
10	443	79.5	125	2	S40344
11	442	79.4	123	2	S35479
12	441	79.2	107	2	A45722
13	440.5	79.1	109	2	A30608
14	440	79.0	129	2	S29627
15	438	78.6	128	2	S40345
16	437	78.5	107	2	S34005
17	436	78.3	106	2	PI0267
18	433.5	77.8	108	2	B30608
19	433.5	77.8	129	2	A32274
20	432.5	77.6	109	2	G30607
21	431.5	77.5	109	1	K3HUT1
22	431	77.4	107	2	S57444
23	430.5	77.3	109	2	D30601
24	430.5	77.3	109	2	C30601
25	429.5	77.1	109	2	H30601
26	429	77.0	128	2	S40343
27	428.5	76.9	109	1	K3HUS1
28	427.5	76.8	109	2	G30601
29	427.5	76.8	109	2	B30601

30	427.5	76.8	128	2	S20636	Ig kappa chain V r
31	427.5	76.8	129	1	K3HUNA	Ig kappa chain pre
32	426.5	76.6	215	2	JE0244	Ig kappa chain NIG
33	425.5	76.4	108	2	C30608	Ig kappa chain V-I
34	424.5	76.2	110	2	S20635	Ig kappa chain V r
35	424.5	76.2	129	2	S49532	Ig kappa chain V r
36	423.5	76.0	109	2	PH0963	anti-sm antibody V
37	423.5	76.0	109	2	PH0963	Ig kappa chain V r
38	422.5	75.9	109	2	K3HUTL	Ig kappa chain V-I
39	422.5	75.9	129	1	K3HUTL	Ig kappa chain pre
40	420	75.4	114	2	S46375	Ig kappa chain V-J
41	419.5	75.3	130	2	S40360	Ig kappa chain - h
42	419	75.2	138	2	A26471	Ig kappa chain pre
43	417.5	75.0	109	2	F30601	Ig kappa chain V-I
44	417.5	75.0	129	2	S46369	Ig light chain var
45	417.5	75.0	134	2	S38643	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PI0106 Ig kappa chain precursor V-J-C region (LSI) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PI0106

R:Silberstein, L.E., Litvin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A:Reference number: PI0106; MUID:89235583

A:Accession: PI0106

A:Molecule type: mRNA

A:Residues: 1-144 <STL>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match

Best Local Similarity 84.4%; Score 470; DB 2; Length 144;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSQASQSIHNLHWYQORPOAPRLTLXYSQSIGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSQASQSVSSITLAWYQORPOAPRLTLXYSQSIGIPA 80

Qy 61 RFSSGSGTDFTLTISLSEPEDFAVYICQSGSPHPTFGGGRVKEIK 107

Db 81 RFSSGSGTDFTLTISLSEPEDFAVYICQSGSPHPTFGGGRVKEIK 127

RESULT 2

S23628 Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23628

R:O'Lee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A

J. Exp. Med. 175, 833-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A:Reference number: S23623; MUID:92156804

A:Accession: S23628

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-111 <OLE>

A:Cross-references: EMBL:X59705; NID:g34022; PIDD:CAAA2226.1; PTD:g1335150
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match	82.6%	Score 460;	DB 2;	Length 111;
Best Local Similarity	83.2%;	Pred. No. 9.3e-35;		
Matches	89;	Conservative	7;	Mismatches 11; Indels 0; Gaps 0;

```
QY      1 EIVLTOSPATLSLSPGERATLSGCAQSQTSHHLHWQQRPGAPRLLLXRSQSLSGIPA 60
        |||||||.....:::|||||.....|-::::|
DB       1 EIVLTOSPATLSLSPGERATLSGRASQSVSYLAWYQKPGCAPRLLLIDASNRAITGIPA 60
```

```
QY      61 RFSGSGGTDTLTLSLEPEDFAVYYCCQGSGSWPHTFGGGKTKVEIK 107  
       |||||  
Db      61 RFSGSGGTDTLTLTSSLEPEDFAVYYCQQRSMWPWTFGGCKTKEIK 107
```

RESULT 3
A56701
Ig kappa chain V region precursor (Hs) - human (fragment)

C:\Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:\Accession: A56701
R.Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995

(with 1 additional page) will be added to blood group & antibodies

A:Accession: A56701

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <NIC>

A:Cross-references: GB:LA1174; NID:g762823; PIDD:AA64877.1; PID:g762822
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:36-110/Domain: immunoglobulin homology <IMD>

Query Match	82.28;	Score 458;	DB 2;	Length 128;
Best Local Similarity	82.28;	Pred. No. 1.6e-34;		
Matches 88;	Conservative	11;	Indels	0;
			Gaps	0

```
QY      1 EIVLTGSPATLSLSPGERATLSCAQSQISNHLHWYQQRPGAPELLTXRSGSISGIPA   60
        |||||
        |:::|||||
        :|||
Db     21 EIVLTGPSATLSLSPGERATLSCRAQSQSVSYLAWYQQKPGAPRLLIYDASNRRGTGIP   80
```

```

QY      61 RFGSGSGTDFLTLTSSLEPEDFAVYYCQSGSWPHTEGGGKYEK 107
      |||||
      81 RFGSGSGTDFLTLTSSLEPEDFAVYYCQGRSNWPRSGGQGTKEIK 127
      |||||
      Db

```

RESULT 4
S40379
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40379
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23: 3248-3271, 1993

A:Reference number: S40312; MUID:94080891
A:Accession: S40379
A:Status: preliminary; translation not shown
A:Title: Expressed human immunoglobulin cni genes and their hypermutation.

A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72489; NID:g4441446; PIDN:CA51157.1; PID:g441447
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin F₃₆₋₁₁₀/Domain: immunoglobulin homology <IMM>

```
query match      82.0%; score 457; DB 2; length 128;
```

Best Local Similarity 81.3%; Pred. No. 2e-34;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

```

QY      1 EIVLTSPATLSLSPGERATLSCQASQSTSNHLMHWYQQRPGCAPRLLIYRSQSIQIPA 600
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      21 EFVLTSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQPRLLIYYASNRATGIPA 800

```

```

QY      61  RFGSGSGTDTLTLTSSLEPEDFAVYYCQSGSWPHTEGGGTKEIK 107
      |||||:|||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      81  RFGSGAGTDTLTLTSSLEPEDFAVYYCQGRSKWPWTEGGGTKEIK 127

```

RESULT	5
S54905	
Ig kappa chain V region - human (fragment)	
Accession: U08670 (EMBL)	

C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S54905.1
R:Esposito, G.; Traboni, C.
Submitted to the EMBL Data Library November 1994

A:Description: Cloning and sequencing of CDNA coding for the variable domains of a mu
A:Reference number: S54905
A:Accession: S54905
A:Status: preliminary

A: Molecule type: mRNA
A: Residues: 1-114 <ESP>
A: Cross-references: EMBL:X82934; NID:g809554; PIDD:CA58108.1; PID:g809555
C: Superfamily: immunoglobulin V region: immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match	81.2%;	Score 452.5;	DB 2;	Length 114;
Best Local Similarity	80.68;	Pred. No. 4.5e-34;		
Matches	87;	Conservative	11;	Mismatches 9;
				Indels 1;
				Gaps 1;

```

0y      1 EIVLTSPATLSLSPGERATLSCQASQSIJNHLHWYQQRPGCAPRLLLXYRSGSISGIPA 600
        :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 DVVMTQSPATLSLSPGERATLSCRASQSVSYLVHWYQQRPGAPRLLLYDASRATGIPA 600

```

```
Oy      61 RFSGSGSCTDFTLTSSLEPEFAVYYCQOGSWPH-TFGGKTVEIK 1077  
        ||||| | | | | | | |
        |||||  
        ||||| : || |||||  
        |||||  
Db      61 RFSGSGSCTDFTLTSSLEPEFAVYYCQQRSMNPPYTFGGGTKEIK 1089
```

RESULT	6
G44151	
Ig kappa chain V region (JM-10) - human (fragment)	

CjDate: 27-Jun-1994 #sequence_revision 27-Jun-1994 #tex_change 21-Jan-2000
CjAccession: C64151
Rizebadee, S.L.; Barbas, III, C.F.; Hom, Y.L.; Coathien, R.H.; Graff, R.; Degraw, J.

A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.	
A:Reference number: A44151; MUID:92228746	
A:Accession: G44151	
A:Abstract: This paper reports on the construction of a not combinatorial with conceptual framework of antibody libraries.	

A:Note: nucleotide translation not given
A:Cross-references: NID:g1833968; PIDN:AAA35975.1; PID:g1833969
A:Residues: 1-108 (CB:M88317; NID:g1833968; PIDN:AAA35975.1; PID:g1833969)
A:Molecule type: mRNA

C:superfamily::immunoglobulin V region; immunoglobulin homology
C:keywords: heterotetramer; immunoglobulin
F,15-89/Domain::immunoglobulin homology <IMM>

Query.Match	81.08;	Score 451;	DB 2;	Length 108;
Best Local Similarity	82.78;	Pred. No. 5.8e-34;		
Matches: 86;	Conservative 8;	Mismatches 10;	Indels 0;	Gaps 0;

```
Oy      4 LTGPATLSTSPGERATLSCQASOSISNHLHWYORPGGAPELLIXRSOSIGSIPARFS    63  
        |||||  
Db      3 LTGSATLSTSPGERATLSCRASQSVSYLAWYOQKPGAARLLIYDASNRAIGIPARFS    62
```

OY 64 GSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 107
|||||
DB 63 GSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 106

RESULT 7

PC4282
Ig kappa chain (anti-ss-A/Ro 60k peptide) (E-42 and E-56) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C:Accession: PC4282; PC4284
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kasaiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin
A:Reference number: PC4279; MUID:97236289
A:Accession: PC4282
A:Molecule type: protein
A:Residues: 1-106 <SD2>
A:Note: E-42
A:Accession: PC4284
A:Molecule type: protein
A:Residues: 1-106 <SD2>
A:Note: E-56
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogers
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 447; DB 2; Length 106;
Best Local Similarity 81.0%; Pred. No. 1.3e-33;

Matches 85; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

OY 3 VLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 62
|||||
DB 1 VLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 60

OY 63 GSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 107
|||||
DB 61 GSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 105

RESULT 8

B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: B45722; MUID:93100833
A:Accession: B45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCHI backbone (NCBIR:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 447; DB 2; Length 107;
Best Local Similarity 75.7%; Pred. No. 1.3e-33;

Matches 81; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

OY 1 EIVLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 60
|||||
DB 1 DIVLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 60
OY 61 RFSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 107
|||||
DB 61 RFSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 107

RESULT 9

S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40362
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: EMBL:X72472; NID:g441412; PID:g441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 444; DB 2; Length 117;
Best Local Similarity 79.4%; Pred. No. 2.7e-33;

Matches 85; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

OY 1 EIVLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 60
|||||
DB 11 EIVLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 70

OY 61 RFSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 107
|||||
DB 71 RFSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 117

RESULT 10

S40344
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40344
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40344
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72454; NID:g441376; PID:CA51122.1; PID:g441377
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 443; DB 2; Length 125;
Best Local Similarity 81.9%; Pred. No. 3.5e-33;

Matches 86; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 EIVLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 60
|||||
DB 21 EIVLTOSPATLISPERATLSCQASQISNHLHWYQORPOAPRLIXRSQISGIPARF 80

OY 61 RFSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 105
|||||
DB 81 RFSGSGTDFLTITSSLEPEDFAVYVCOQSGSWPHFGGKTVEIK 125

RESULT 11

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

A:Accession: S40345
A:Status: preliminary; translation not shown

A: Molecule type: mRNA
 A: Residues: 1-128 <KLE>
 A: Cross-references: EMBL:X72455; NID:g441378; PIDN:CA51123.1; PID:g441379
 C: Superfamily: immunoglobulin V region; immunoglobulin homology
 C: Keywords: heterotetramer; immunoglobulin
 F: 32-106/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 438; DB 2; Length 128;
 Best Local Similarity 78.9%; Pred. No. 1e-32;
 Matches 86; Conservative 8; Mismatches 13; Indels 2; Gaps 1;
 QY 1 EIVLTQSPATISLSPGERATISCOAQSISNHLHWYQORPGQAPRLIXYRSQISGIPA 60
 |||||
 DB 17 EIVLTQSPATISLSPGERATISCRASQSVRIYAWYQORPGQAPRLITYDAINRATGIPA 76
 |||||
 QY 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCOQSGSMPH--TFGGGTVEIK 107
 |||||
 DB 77 RFSGSGSGTDFTLTITSSLEPEDFAVYYCOQSGSNMPPLTFGGGTVEYK 125
 |||||

Search completed: February 13, 2001, 09:04:14
 Job time: 78 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:23:11 ; Search time 14.89 Seconds
(without alignments)
232.066 Million cell updates/sec

Title: US-08-790-540A-4

Perfect score: 357
Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHTFGGKTKEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	431.5	77.5	109 1	KV3D_HUMAN P01622 homo sapien
2	428.5	76.9	109 1	KV3B_HUMAN P01620 homo sapien
3	427.5	76.8	129 1	KV3L_HUMAN P18135 homo sapien
4	422.5	75.9	109 1	KV3E_HUMAN P01623 homo sapien
5	422.5	75.9	129 1	KV3M_HUMAN P18136 homo sapien
6	418.5	75.1	129 1	KV3H_HUMAN P04207 homo sapien
7	413	74.1	115 1	KV3I_HUMAN P04433 homo sapien
8	410.5	73.7	109 1	KV3F_HUMAN P01624 homo sapien
9	406.5	73.0	108 1	KV3A_HUMAN P01619 homo sapien
10	406	72.9	128 1	KV3K_HUMAN P06311 homo sapien
11	402.5	72.3	109 1	KV3G_HUMAN P04206 homo sapien
12	380	68.2	108 1	KV1M_HUMAN P01605 homo sapien
13	373	67.0	108 1	KV1H_HUMAN P01600 homo sapien
14	371	66.6	111 1	KV3H_MOUSE P01660 mus musculu
15	370	66.4	108 1	KV1J_HUMAN P80362 homo sapien
16	370	66.4	111 1	KV3L_MOUSE P01664 mus musculu
17	370	66.4	111 1	KV3R_MOUSE P01670 mus musculu
18	367.5	66.0	116 1	KV3J_HUMAN P04434 homo sapien
19	367	65.9	129 1	KV1E_HUMAN P04431 homo sapien
20	366	65.7	108 1	KV1E_HUMAN P01597 homo sapien
21	365.5	65.6	100 1	KV3C_HUMAN P01621 homo sapien
22	365	65.5	108 1	KV1P_HUMAN P01608 homo sapien
23	365	65.5	108 1	KV1V_HUMAN P04430 homo sapien
24	365	65.5	115 1	KV5I_MOUSE P01642 mus musculu
25	365	65.5	134 1	KV4C_HUMAN P06314 homo sapien
26	364.5	65.4	133 1	KV4B_HUMAN P06313 homo sapien
27	364	65.4	111 1	KV3J_MOUSE P01662 mus musculu
28	364	65.4	111 1	KV3T_MOUSE P01672 mus musculu
29	364	65.4	114 1	KV4A_HUMAN P01625 homo sapien
30	363	65.2	111 1	KV3U_MOUSE P01673 mus musculu
31	362	65.0	108 1	KV1G_HUMAN P01599 homo sapien
32	361	64.8	111 1	KV3M_MOUSE P01665 mus musculu
33	360	64.6	108 1	KV1N_HUMAN P01606 homo sapien

34	360	64.6	111 1	KV3Q_MOUSE P01667 mus musculu
35	360	64.6	131 1	KV3I_MOUSE P01661 mus musculu
36	359	64.5	108 1	KV1K_HUMAN P01603 homo sapien
37	359	64.5	111 1	KV3S_MOUSE P01671 mus musculu
38	358	64.3	108 1	KV1B_HUMAN P01594 homo sapien
39	358	64.3	108 1	KV1R_HUMAN P01610 homo sapien
40	358	64.3	107 1	KV3D_MOUSE P03977 mus musculu
41	357.5	64.2	107 1	KV3D_MOUSE P01596 homo sapien
42	357	64.1	108 1	KV1O_HUMAN P01607 homo sapien
43	357	64.1	108 1	KV1S_HUMAN P01611 homo sapien
44	357	64.1	111 1	KV3N_MOUSE P01666 mus musculu
45	357	64.1	111 1	KV3Q_MOUSE P01669 mus musculu

ALIGNMENTS

RESULT 1
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622:
DT 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
RN PIR: A01895; K3HTI.
RP HSSP: P01789; 2MCP.
RX MEDLINE-72188439; PubMed-5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein T1). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HTI.
DR HSSP: P01789; 2MCP.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CUC749BC CRC64;

Query Match 77.5%; Score 431.5; DB 1; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.8e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

OY 1 EIVLTQSPATLSLSPGERATLSCAQSISN-ELHWYQRPQADRLIYXSQISGIP 59
DB 1 EIVLTQSPATLSLSPGERATLSCRAQSISN-ELHWYQRPQADRLIYXSQISGIP 60
OY 60 ARFGSGSGTDFLTLSLEPEDFAVYCCQSGSWPHTFGGKTKEIK 107
DB 61 DRFGSGSGTDFLTLSLEPEDFAVYCCQSGSWPHTFGGKTKEIK 108

RESULT 2
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620:
DI 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION SI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

[1]
 RN SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human Igm anti-gamma-globulins of the wa
 RT group."
 RL Biochemistry 20:5816-5822(1981).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01892; K3HUS1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 15; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match
 Best Local Similarity 76.9%; Score 428.5; DB 1; Length 109;
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

OY 1 EIVLTGSPATLSLSPERATLSCQASQISN-HLHWYQRPQAPRLLIYRSQISGIP 59
 DB 1 EIVLTGSPATLSLSPERATLSCQASQISN-HLHWYQRPQAPRLLIYRSQISGIP 60
 OY 60 ARSSGSGSDFTLTITSLPEPFAVYVCOQSGSNPHTEGGGTKEIK 107
 DB 61 DRFSGSGSDFTLTITSLPEPFAVYVCOQSGSNPHTEGGGTKEIK 108

RESULT 3
 KY3L_HUMAN STANDARD; PRT: 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: P10022; K3HUA.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 15; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129
 FT DOMAIN 21 43
 FT DOMAIN 44 55
 FT DOMAIN 56 70
 FT DOMAIN 71 77
 FT DOMAIN 78 109
 FT DOMAIN 110 118
 FT DOMAIN 119 129
 FT DISULFID 43 109
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3G5529272774D0 CRC64;

Query Match
 Best Local Similarity 76.8%; Score 427.5; DB 1; Length 129;
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

OY 1 EIVLTGSPATLSLSPERATLSCQASQISN-HLHWYQRPQAPRLLIYRSQISGIP 59
 DB 21 EIVLTGSPATLSLSPERATLSCQASQISN-HLHWYQRPQAPRLLIYRSQISGIP 80
 OY 60 ARSSGSGSDFTLTITSLPEPFAVYVCOQSGSNPHTEGGGTKEIK 107
 DB 81 DRFSGSGSDFTLTITSLPEPFAVYVCOQSGSNPHTEGGGTKEIK 128

RESULT 4
 KY3E_HUMAN STANDARD; PRT: 109 AA.
 AC P01623;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION WOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human Igm anti-gamma-globulins of the wa
 RT group."
 RL Biochemistry 20:5816-5822(1981).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01896; K3HUS1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 15; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11746 MW; 566C115EB9CEEE CRC64;

Query Match
 Best Local Similarity 75.9%; Score 422.5; DB 1; Length 109;
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

OY 1 EIVLTGSPATLSLSPERATLSCQASQISN-HLHWYQRPQAPRLLIYRSQISGIP 59
 DB 1 EIVLTGSPATLSLSPERATLSCQASQISN-HLHWYQRPQAPRLLIYRSQISGIP 60
 OY 60 ARSSGSGSDFTLTITSLPEPFAVYVCOQSGSNPHTEGGGTKEIK 107
 DB 61 DRFSGSGSDFTLTITSLPEPFAVYVCOQSGSNPHTEGGGTKEIK 108

RESULT 5
 KY3M_HUMAN STANDARD; PRT: 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

RF "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RL mutation. Implications for etiology and immunotherapy.";
 CC J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC PIR: P10021; K3H0H1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 75.9%; Score 422.5; DB 1; Length 129;
 Best Local Similarity 79.6%; Pred. No. 1.9e-37;
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGAPRLILYXSQISGIP 59
 DB 21 EIVLTQSPATLSLSPGERATLSCRASQSYSSNIAYCOQPGAPRLILYGASTRATGIPA 80
 QY 60 AREFSGSGSTDTLTLSLEPEDFAYVYCOQSGSMPTGGGKYEIK 107
 DB 81 RRFSGSGSTDTLTLSLEPEDFAYVYCOQSGSMPTGGGKYEIK 128

RESULT 6

KV3H_HUMAN STANDARD; PRT; 129 AA.

AC P04207;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION CCL PRECURSOR (RHEUMATOID FACTOR).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86177570; PubMed-3083417;
 RA Jirik F.R., Sogge J., Fong S., Heltzmann J.G., Cui J.G., Chen P.P.,
 RA Goldstein R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).

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CC EMBL: M12740; AAA58992.1; -
 DR PIR: A01898; K3H0H1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g: 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CCL.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 75.1%; Score 418.5; DB 1; Length 129;
 Best Local Similarity 75.9%; Pred. No. 4.8e-37;
 Matches 82; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGAPRLILYXSQISGIPA 60
 DB 21 EIVLTQSPATLSLSPGERATLSCRASQSYSSNIAYCOQPGAPRLILYGASTRATGIPA 80
 QY 61 RREFSGSGSTDTLTLSLEPEDFAYVYCOQSGSM-PTGGGKYEIK 107
 DB 81 RRFSGSGSGTEFTLTSLRQSEDFAYVYCOQYNNMPTGGGKYEIK 128

RESULT 7

KV3I_HUMAN STANDARD; PRT; 115 AA.

AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-85087932; PubMed-6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus.";
 RT Nucleic Acids Res. 12:9229-9236(1984).
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 CC or send an email to license@sib-sib.ch).

CC EMBL: X01668; -; NOT_ANNOTATED_CDS.
 DR PIR: A01900; K3H0VG.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g: 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A1D555 CRC64;

Query Match

74.1%; Score 413; DB 1; Length 115;

Best Local Similarity 83.2%; Pred. No. 1.6e-36;
Matches 79; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 60
DB 21 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 80

QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMP 95
DB 81 RFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMP 115

RESULT 8

KV3F_HUMAN STANDARD; PRT; 109 AA.

AC P01624;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN V-III REGION POM.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RESULT 10

KV3K_HUMAN STANDARD; PRT; 128 AA.

AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RESULT 9

KV3A_HUMAN STANDARD; PRT; 108 AA.

AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Query Match 73.7%; Score 410.5; DB 1; Length 109;
Best Local Similarity 75.0%; Pred. No. 2.7e-36;
Matches 81; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 59
DB 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 60

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

RESULT 10

KV3K_HUMAN STANDARD; PRT; 128 AA.

AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RESULT 9

KV3A_HUMAN STANDARD; PRT; 108 AA.

AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Query Match 73.0%; Score 406.5; DB 1; Length 108;
Best Local Similarity 73.1%; Pred. No. 7.1e-36;
Matches 79; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 59
DB 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 60

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

RESULT 10

KV3K_HUMAN STANDARD; PRT; 128 AA.

AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RESULT 9

KV3A_HUMAN STANDARD; PRT; 108 AA.

AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Query Match 72.9%; Score 406; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 9.7e-36;
Matches 80; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 59
DB 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITXYSQSIGIPA 60

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

QY 60 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 107
DB 61 ARFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSMPHFGGKYEIK 108

CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

```
Matches 70; Conservative 20; Mismatches 17; Indels 0; Gaps 0;
```

OY	1	EVLVLTOSPATLISLSPGERATLSLSCAQSOSQSISSNHLHWYQQRPQAPRLILXYSQSISGIPA	60
Dd	1	DIQMOTSPBSSLASVGDRRTITTCRASQSISSLSLSTWQAQPGAPQVLLTAAASSLPBGVS	60
OY	61	RFSGGSGGTDFTLTITSLEPEDFAVVYYCOQSGSWPTEFGTGKVEIK	107
Dd	61	RFSGGSGGTDFTLTITSLEPEDFAVVYYCOQSNVTTPTSFQGTRVEIK	107
<hr/>			
RESULT	14		
KV3H_MOUSE		STANDARD;	PRT; 111 AA.
ID	KV3H_MOUSE		
AC	P01660;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-II REGION PC 3741/TEPC 111.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
NC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
PN	[1]		
RP	SEQUENCE (PC 3741).		
RX	MEDLINE=79073152; PubMed=103003;		
RA	Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;		
RT	"Rearrangement of genetic information may produce immunoglobulin		
RT	diversity.";		
RL	Nature 276:785-790(1978).		
RN	[2]		
RP	SEQUENCE (TEPC 111).		
RX	MEDLINE=J9012520; PubMed=99744;		
RA	McKeane D.J., Bell M., Potter M.;		
RT	"Mechanism of antibody diversity: multiple genes encode structurally		
RT	related mouse kappa variable regions.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).		
CC	-I- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.		
DR	PIR: A01934; KVM637.		
DR	INTERPRO: IPR003006; -.		
FW	PFAM: PF00047; Ig: 1.		
KW	Immunoglobulin V region.		
FT	DOMAIN	1	23
FT	DOMAIN	24	38
FT	DOMAIN	39	53
FT	DOMAIN	54	60
FT	DOMAIN	61	92
FT	DOMAIN	93	101
FT	DOMAIN	102	111
FT	DISULFD	23	92
FT	NON_TER	111	
SQ	SEQUENCE	111 AA; 12099 MW; EC46C9D259213BE4 CRC64;	
<hr/>			
Query Match	66.6%;	Score 371;	DB 1; Length 111;
Best Local Similarity	64.0%;	Pred. No. 3.7e-32;	
Matches	71; Conservative	19; Mismatches	17; Indels 4; Gaps 1.
OY	1	EVLVLTOSPATLISLSPGERATLSLSCAQSOSQSISSNHLHWYQQRPQAPRLILXYSQSIS	56
Dd	1	DIVLVQSPASLAVALSAGQRATISCRASESVDYSGNSPMHMVQGRKPQPPLILLIRASNLES	60
OY	57	GIPARFSGSGGTDFTLTITSLEPEDFAVVYYCOQSGSWPHTEFGTGKVEIK	107
Dd	61	GIPARFSGSGSRTDFTLITINPEADVAVAYCOQSNEDPYTGGGKTKEIK	111
<hr/>			
RESULT	15		
KVLY_HUMAN		STANDARD;	PRT; 108 AA.
ID	KVLY_HUMAN		
AC	P80362;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-I REGION WAT.		

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN	[1]
RP	SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA	MEDLINE=95086080; PubMed=7993911;
RX	Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultiz M.,
RA	Solomon A., Stevens F.J., Schiffer M.;
RT	"Comparison of crystal structures of two homologous proteins:
RT	structural origin of altered domain interactions in immunoglobulin
RL	light chain dimers.";
RL	Biochemistry 33:14848-14857(1994).
RN	[2]
RP	SEQUENCE OF 1-35.
RX	MEDLINE=81267384; PubMed=6167731;
RA	Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA	Popp R.A., Solomon A.;
RT	"Characterization and preliminary crystallographic data on the VL-
RT	related fragment of the human kappa Bence Jones protein wat.";
RL	J. Mol. Biol. 147:185-193(1981).
CC	-I- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR	PDB: 1WTL; 01-NOV-94.
DR	INTERPRO: IPR003006; -.
DR	PFAM: PF00047; 19; 1.
KW	Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT	DOMAIN 1 23 FRAMEWORK 1.
FT	DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 35 49 FRAMEWORK 2.
FT	DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 57 68 FRAMEWORK 3.
FT	DOMAIN 69 97 COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 98 107 FRAMEWORK 4.
FT	DISULFID 23: 88 BY SIMILARITY.
FT	CONFLICT 30 31 TN -> SD (IN REF. 2).
FT	NON_TER 108 108
SQ	SEQUENCE 108 AA; 11737 MW; D9D941B30FDE697 CXC64;

[illegible]

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Search completed: February 13, 2001, 09:23:12
Job time: 1191 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:04:56 ; Search time 39.42 Seconds
(without alignments)
318.144 Million cell updates/sec

Title: US-08-790-540a-4
Perfect score: 557
Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHFGGRTVEIK 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:***
2: SP bacteria:***
3: SP fungi:***
4: SP human:***
5: SP invertebrate:***
6: SP mammal:***
7: SP mhc:***
8: SP organelle:***
9: SP phage:***
10: SP plant:***
11: SP rodent:***
12: SP virus:***
13: SP vertebrate:***
14: SP unclassified:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	429.5	77.1	109	4 Q9UL85	Q9UL85 homo sapien
2	428	76.8	108	4 Q9UL83	Q9UL83 homo sapien
3	427.5	76.8	109	4 Q9UL78	Q9UL78 homo sapien
4	402.5	72.3	109	4 Q9UL86	Q9UL86 homo sapien
5	385	69.1	108	4 Q9UL77	Q9UL77 homo sapien
6	372	66.8	108	4 Q9UL79	Q9UL79 homo sapien
7	366	65.7	108	4 Q9UL70	Q9UL70 homo sapien
8	362.5	65.1	107	4 Q9UL81	Q9UL81 homo sapien
9	338.5	60.8	106	5 Q9UL10	Q9UL10 schistosoma
10	334	60.0	99	11 Q9UL74	Q9UL74 mus musculu
11	334	60.0	107	11 Q9UL84	Q9UL84 mus musculu
12	332	59.6	298	11 Q9ULF0	Q9ULF0 mus musculu
13	331	59.4	214	11 Q9ULA5	Q9ULA5 mus musculu
14	326	58.5	101	11 Q9UL78	Q9UL78 mus musculu
15	314	56.4	103	11 Q9UL80	Q9UL80 mus musculu
16	309	55.5	97	11 Q9UL76	Q9UL76 mus musculu
17	309	55.5	114	4 Q9UL80	Q9UL80 homo sapien
18	307.5	55.2	104	11 Q9UL82	Q9UL82 mus musculu
19	280	50.3	109	6 Q9N0M5	Q9N0M5 oryctolagus

20	237	42.5	107	4 Q9UL82	Q9UL82 homo sapien
21	217.5	39.0	107	4 Q9NSD6	Q9NSD6 homo sapien
22	168	30.2	130	4 Q9NP29	Q9NP29 homo sapien
23	150.5	27.0	123	4 Q9UK13	Q9UK13 homo sapien
24	150	26.9	93	4 Q9UL76	Q9UL76 homo sapien
25	146	26.2	123	11 Q61243	Q61243 mus musculu
26	134	24.1	168	4 Q9U056	Q9U056 homo sapien
27	134	24.1	246	4 Q9U055	Q9U055 homo sapien
28	126	22.6	342	13 Q9IB00	Q9IB00 spheroides
29	124.5	22.2	334	13 Q9IB05	Q9IB05 spheroides
30	123.5	22.2	309	11 Q9WTN4	Q9WTN4 mus musculu
31	123.5	22.2	509	11 Q9H807	Q9H807 mus musculu
32	121.5	21.8	210	6 P79336	P79336 felis silve
33	119	21.4	152	13 Q9YH11	Q9YH11 ginglymosto
34	118	21.2	100	6 Q77624	Q77624 bos taurus
35	117	21.0	119	4 Q9UL84	Q9UL84 homo sapien
36	115.5	20.7	509	11 Q9QX57	Q9QX57 mus musculu
37	115.5	20.7	513	11 P97797	P97797 mus musculu
38	115.5	20.6	100	13 Q9YH19	Q9YH19 ginglymosto
39	115	20.6	340	13 Q9IAZ6	Q9IAZ6 spheroides
40	114	20.5	333	13 Q9IB04	Q9IB04 spheroides
41	113.5	20.4	336	13 Q9YH09	Q9YH09 ginglymosto
42	113	20.3	136	13 Q9YH16	Q9YH16 ginglymosto
43	113	20.3	340	13 Q9IAZ0	Q9IAZ0 spheroides
44	112.5	20.2	116	4 Q9UL89	Q9UL89 homo sapien
45	112	20.1			

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	109 AA.
Q9UL85	Q9UL85			
AC	Q9UL85			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-98277139; PubMed-9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.,			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035029; RAD56265.1; -.			
DR	HSSP; P01607; IREI.			
DR	INTERPRO; IPR003006; -.			
DR	PFAM; PF00047; 19; 1.			
FT	NON TER			
FT	NON TER			
SO	SEQUENCE			
	109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;			

Query Match 77.1%; Score 429.5; DB 4; Length 109;
Best Local Similarity 78.7%; Pred. No. 8.8e-41;
Matches 85; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY	1 EIVLTQSPATLSLSPGERATISCAQASISNHLHWYQRPQADRLIIYRSQISGIPA 60	
DB	1 EIVLTQSPATLSLSPGERATISCAQASISNHLHWYQRPQADRLIIYRSQISGIPA 60	
QY	61 RFSGSGGTFTLTLSISLEPEDFAVYYCCQSGSPH-TFGGRTVEIK 107	
DB	61 RFSGSGGTFTLTLSISLEPEDFAVYYCCQSGSPH-TFGGRTVEIK 108	

RESULT 2
 Q9UL83 PRELIMINARY: PRT: 108 AA.
 AC Q9UL83:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035031; AAD56267.1; -
 DR HSSP: P01607; 1RET
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1; 1.
 FT NON_TER 1
 FT 108
 SO SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA965EA CRC64;

Query Match 76.8%; Score 428; DB 4; Length 108;
 Best Local Similarity 76.6%; Pred. No. 1.3e-40;
 Matches 82; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLQSPATLSISPERATLSCQASQSI-SNHLHMYOQRPGQAPRLIYXSQISGIP 60
 DB 1 EIVLQSPATLSISPERATLSCQASQSI-SNHLHMYOQRPGQAPRLIYXSQISGIP 60
 QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQSGSNPHFTFGGKTVEIK 107
 DB 61 RFSGSGSGTDFTLTISLSEPEDFAVYVYCOQSGSNPHFTFGGKTVEIK 107

RESULT 3
 Q9UL78 PRELIMINARY: PRT: 109 AA.
 AC Q9UL78:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035036; AAD56272.1; -
 DR HSSP: P01789; 1MCP
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1; 1.
 FT NON_TER 1
 FT 109
 SO SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 76.8%; Score 427.5; DB 4; Length 109;
 Best Local Similarity 80.6%; Pred. No. 1.5e-40;

Matches 87; Conservative 6; Mismatches 14; Indels 1; Gaps 1;
 QY 1 EIVLQSPATLSISPERATLSCQASQSI-SNHLHMYOQRPGQAPRLIYXSQISGIP 59
 DB 1 EIVLQSPATLSISPERATLSCQASQSI-SNHLHMYOQRPGQAPRLIYXSQISGIP 60
 QY 60 ADFSGSGTDFTLTISLSEPEDFAVYVYCOQSGSNPHFTFGGKTVEIK 107
 DB 61 DFFSGSGTDFTLTISLSEPEDFAVYVYCOQSGSNPHFTFGGKTVEIK 108

RESULT 4
 Q9UL86 PRELIMINARY: PRT: 109 AA.
 AC Q9UL86:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035028; AAD56264.1; -
 DR HSSP: P01789; 1MCP
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1; 1.
 FT NON_TER 1
 FT 109
 SO SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 72.3%; Score 402.5; DB 4; Length 109;
 Best Local Similarity 76.9%; Pred. No. 9.3e-38;
 Matches 83; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 1 EIVLQSPATLSISPERATLSCQASQSI-SNHLHMYOQRPGQAPRLIYXSQISGIP 59
 DB 1 EIVLQSPATLSISPERATLSCQASQSI-SNHLHMYOQRPGQAPRLIYXSQISGIP 60
 QY 60 ADFSGSGTDFTLTISLSEPEDFAVYVYCOQSGSNPHFTFGGKTVEIK 107
 DB 61 DFFSGSGTDFTLTISLSEPEDFAVYVYCOQSGSNPHFTFGGKTVEIK 108

RESULT 5
 Q9UL77 PRELIMINARY: PRT: 108 AA.
 AC Q9UL77:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).

[illegible]

RESULT 9
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MONOCLONAL ANTI-IDIOCYTIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Strigedidae; Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF207620; AAF19434.1; -
DR HSSP: P01679; 2FB;
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
FT NON_TER 1 1
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 60.8%; Score 338.5; DB 5; Length 106;
Best Local Similarity 59.8%; Pred. No. 1.3e-30;
Matches 64; Conservative 18; Mismatches 24; Indels 1; Gaps 1;

QY 1 EIVLTGSPATLSLSPGERATLSCQASQISNHLHWYQORPGAPRLIYXRSQISGIPA 60
DB 1 ENLLTSPALMSASPGKYMTCSSASSVS-YVYWLQKRGSSPRLITDTNLSAGVVP 59
QY 61 RFGSGSGXDTFTLTSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 60 RFGSGSGXDTFTLTSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 106
RESULT 10
Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206032; AAF69330.1; -
FT NON_TER 1 1
SQ SEQUENCE 99 AA; 10939 MW; 3B2D0E78453324 CRC64;

Query Match 60.0%; Score 334; DB 11; Length 99;
Best Local Similarity 61.9%; Pred. No. 3.9e-30;
Matches 60; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 11 LSLSPGERATLSCQASQISNHLHWYQORPGAPRLIYXRSQISGIPARFSGSGGSTD 70
DB 3 LTVASGDRVITICKASQSVSNDAVWYQORPGAPRLIYXRSQISGIPARFSGSGGSTD 62
QY 71 FTLTSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 63 FTTTSTVQEDLAVYFCQODYSPPHTFGGKVEIK 99

RESULT 11
Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206022; AAF69320.1; -
FT NON_TER 1 1
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match 60.0%; Score 334; DB 11; Length 107;
Best Local Similarity 58.9%; Pred. No. 4.3e-30;
Matches 63; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 1 EIVLTGSPATLSLSPGERATLSCQASQISNHLHWYQORPGAPRLIYXRSQISGIPA 60
DB 1 DIOMQSTSLASLGDNRXKXCSAQISNXXMFOGKPDGTVALIYYTSSLSKSGVPS 60
QY 61 RFGSGSGXDTFTLTSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 61 RFGSGSGXDTFTLTSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107

RESULT 12
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CN 8 SCFV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinohara N., Demura T., Fukuda H.;
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C; TISSUE-SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:03:47 ; Search time 26.34 Seconds
(without alignments)
138.904 Million cell updates/sec

Title: US-08-790-540A-4

Perfect score: 557
Sequence: 1 EVLTQSPATLSLSPGERAT.....COQSGSWPTFGGKTRVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 3413795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.*
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17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	99.6	107	19	W76006
2	555	99.6	107	19	W76002
3	506	90.8	107	13	R25729
4	504	90.5	107	20	W84098
5	504	90.5	112	20	W84100
6	501	89.9	127	18	W08946
7	495	88.9	107	18	W08948
8	495	88.9	107	18	W08949
9	490	88.0	107	20	Y30205
10	489	87.8	107	20	Y30203
11	484	86.9	127	21	Y32407
12	480	86.2	127	15	R50192

Result No.	Score	Query Match	Length	ID	Description
13	480	86.2	127	20	Y26982
14	478	85.8	107	14	R37612
15	474	85.1	107	21	Y70604
16	474	85.1	127	15	R50187
17	474	85.1	127	20	Y26980
18	474	85.1	245	21	Y70605
19	471	84.6	127	15	R50191
20	471	84.6	127	20	Y26981
21	464	83.3	107	19	W76004
22	450	80.8	105	20	W87456
23	450	80.8	105	20	W87458
24	449.5	80.7	107	18	W24513
25	449	80.6	109	20	Y06380
26	446	80.1	214	20	Y08599
27	440	79.0	349	12	R12128
28	440	79.0	401	12	R12129
29	440	79.0	414	12	R13111
30	440	79.0	414	12	R13018
31	438	78.6	108	21	Y53774
32	436.5	78.4	108	21	Y53775
33	436.5	78.4	238	21	Y53775
34	434	77.9	109	15	R52033
35	431	77.4	107	14	R38601
36	431	77.4	107	19	W58482
37	431	77.4	108	12	R15438
38	431	77.4	240	12	R15443
39	430	77.2	111	13	R25721
40	429.5	77.1	104	18	W31723
41	429.5	77.1	107	18	W24514
42	429.5	77.1	110	18	W27545
43	429.5	77.1	129	14	R38672
44	427	76.7	107	14	R38593
45	427	76.7	107	19	W58493

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	555	99.6	107	19	W76006
2	555	99.6	107	19	W76002
3	506	90.8	107	13	R25729
4	504	90.5	107	20	W84098
5	504	90.5	112	20	W84100
6	501	89.9	127	18	W08946
7	495	88.9	107	18	W08948
8	495	88.9	107	18	W08949
9	490	88.0	107	20	Y30205
10	489	87.8	107	20	Y30203
11	484	86.9	127	21	Y32407
12	480	86.2	127	15	R50192

LM609 grafted anti light chain variable region protein fragment.

LM609; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; LM609; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.

Mus. sp.

Key difference 49 Location/Qualifiers

Misc-difference 49 /label= Arg, Met

W09833919-A2.

06-AUG-1998.

30-JAN-1998; 98WO-US01826.

30-JAN-1997; 97US-0791391.

(IXSY-) IXSYS INC.

Glaser SM, Huse WD;

WPI; 1998-437472/37.

PT CMV, T-cell disorders, myeloid disorders and auto-immune conditions

Claim 40; Fig 27A; 14pp; English.

CC The sequence shows the humanised mature light chain variable region of the mouse CMV antibody. Murine CDRs were used in a human W01 framework to produce a pure humanised immunoglobulin (Ig) which is capable of binding to the 9H glycoprotein of cytomegalovirus. The Ig is non immunogenic, due to the human framework, and has a strong affinity for its predetermined antigen. They can be produced in large quantities via recombinant DNA and monoclonal antibody technology. The humanised Ig may be used alone or in combination with chemotherapeutic agents such as non-steroidal anti-inflammatory drugs or immunosuppressants. See also R25721-32.

CC Sequence 107 AA;

Query Match 90.8%; Score 506; DB 13; Length 107;
Best Local Similarity 90.7%; Pred. No. 1.3e-32;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATISCAQSOSISNHLHWYQQRPQAPRLILXYRQSISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATISCAQSOSISNHLHWYQQRPQAPRLILXYRQSISGIPA 60
OY 61 RSSGSGSDFTLITSSLEPEFAVYVYCCQSGSMRHTFGGKTKYIK 107
DB 61 RITSGSGSDFTLITSSLEPEFAVYVYCCQSGSMRHTFGGKTKYIK 107

RESULT 4

ID W84098 standard; Protein: 107 AA.

AC W84098;

DT 15-MAR-1999 (first entry)

DE Humanised anti-alpha-v beta-3 Mab D12HZHC 1-0 VL.

KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

KW angiogenesis; diabetic retinopathy; inflammation;

KW macular degeneration; osteoporosis; Paget's disease;

KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

KW D12HZHC-10.

OS Homo sapiens.

OS Synthetic.

OS Key

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

XX WPI: 1999-034590/03.
DR N-PSDB: V71800.
XX
PT New anti alpha-v beta-3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis

PS Claim 2; Page 61-62; 97pp; English.

CC This is the amino acid sequence of the light chain variable region
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence
CC (see W84096) of human Kabat subgroup III kappa chain, with
CC complementarity determining regions (CDRs) from the murine
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D12 (see W84093). 3 Murine framework residues (1, 49 and 60)
CC are retained. The humanised light chain can be expressed in host
CC cells using nucleic acid molecules (see V71800) of the invention.
CC Humanised D12 VL is also provided (see W84097). The humanised
CC antibodies can be used for passive immunotherapy of disorders
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
CC angiogenic-related disorders, such as angiogenesis associated
CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
CC inflammatory disorders, macular degeneration, rheumatoid arthritis
CC and cancer, e.g. solid tumour metastasis, and diseases where bone
CC resorption is associated with pathology such as osteoporosis,
CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
CC osteolytic lesions produced by bone metastasis, bone loss due to
CC immobilisation or sex hormone deficiency. They can also be used for
CC targeted drug therapy, and for detection and diagnosis.

SO Sequence 107 AA;

Query Match 90.5%; Score 504; DB 20; Length 107;
Best Local Similarity 89.7%; Pred. No. 1.9e-32;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATISCAQSOSISNHLHWYQQRPQAPRLILXYRQSISGIPA 60
DB 1 DIVLTQSPATLSLSPGERATISCAQSOSISNHLHWYQQRPQAPRLILXYRQSISGIPA 60
OY 61 RSSGSGSDFTLITSSLEPEFAVYVYCCQSGSMRHTFGGKTKYIK 107
DB 61 RITSGSGSDFTLITSSLEPEFAVYVYCCQSGSMRHTFGGKTKYIK 107

RESULT 5

ID W84100 standard; Protein: 112 AA.

AC W84100;

DT 15-MAR-1999 (first entry)

DE Vitronectin alpha-v beta-3 Mab VL.

KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

KW angiogenesis; diabetic retinopathy; inflammation;

KW macular degeneration; osteoporosis; Paget's disease;

KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

OS Mus sp.

OS W09840488-A1.

FT 17-SEP-1998.

FT 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.
 PR (SMIK) SMITHKLINE BEECHAM CORP.
 PA Johnson KO, Jonak ZL, Taylor AH;
 PI WPI; 1999-034590/03.
 XX N-PSDB; V71802.
 DR
 XX
 PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, stenosis, cancers or
 PT osteoporosis
 PS
 XX Example 13; Page 64; 97pp; English.
 CC This is the amino acid sequence of the region of the murine
 CC monoclonal antibody (Mab) D12 light chain variable region (VL)
 CC that is altered in humanised D12 VL (see also W84098). A
 CC synthetic gene (see V81902) encoding the protein was prepared
 CC from synthetic oligonucleotides and used to prepare an expression
 CC vector for humanised D12 VL. D12 is an anti-human alpha_v beta_3
 CC vitronectin receptor Mab. Humanised D12 Mabs can be used for
 CC passive immunotherapy of disorders mediated by the alpha_v beta_3
 CC vitronectin receptor, e.g. stenosis and angiogenic associated
 CC diseases.
 CC
 XX
 SQ Sequence 112 AA:

Query Match 90.5%; Score 504; DB 20; Length 112;
 Best Local Similarity 89.7%; Pred. No. 2e-32;
 Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPGAPRLIYRSGISGIPA 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 divltqspatlsispgeratlsqcrasqisnlnhwyqqrpgaprlilkyasqisgipds 60
 OY 61 RFGSGSGTDFLTLLTSSLEPEDFAVYVYCOQSGSWPHTFGGTFVEIK 107
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 rfsqsgsgtdftlltsslepedfavyvycqsgswphtfggtfveik 107

RESULT 6
 W08946
 ID W08946 standard; Protein; 127 AA.

AC W08946;

DT 18-SEP-1997 (first entry)

DE Kappa light chain variable region of 225RA antibody.

KW Kappa; light chain; reshaped; monoclonal; antibody; 225RA;
 KW human; epidermal growth factor; EGF; receptor; inhibition; growth;
 KW tumour; cell; late stage; prostatic; prostate; variable region.

OS Homo sapiens.

PN W09640210-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US09847.

PR 15-DEC-1995; 95US-0573289.

PR 07-JUN-1995; 95US-0482982.

PA (IMCL-) IMCLONE SYSTEMS INC.

PA (MRC-) MRC COLLABORATIVE CENT.
 PI Giergio NA, Goldstein NI, Jones ST, Saldanha JW;

XX WPI; 1997-051897/05.
 DR N-PSDB; T49345.
 XX
 PT Chimeric and humanised versions of anti-EGF receptor antibody 225 -
 PT used for inhibiting tumour growth, esp. of late stage prostatic
 PT tumour
 PS
 XX Claim 31; Fig 19; 112pp; English.
 CC The present sequence is the kappa light chain variable region
 CC of the reshaped human monoclonal antibody (Mab) H225, 225RA. The
 CC Mab is specific for the human epidermal growth factor (EGF)
 CC receptor.
 CC The Mab, or a fragment, can be used to inhibit the growth of tumour
 CC cells, especially late stage prostatic tumour cells in humans,
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle
 CC inhibitor.
 CC
 XX
 SQ Sequence 127 AA:

Query Match 89.9%; Score 501; DB 18; Length 127;
 Best Local Similarity 88.8%; Pred. No. 3.7e-32;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPGAPRLIYRSGISGIPA 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 21 elvltqspatlsispgeratlsqcrasqisnlnhwyqqrpgaprlilkyasqisgipds 80
 OY 61 RFGSGSGTDFLTLLTSSLEPEDFAVYVYCOQSGSWPHTFGGTFVEIK 107
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 81 rfsqsgsgtdftlltsslepedfavyvycqsgswphtfggtfveik 127

RESULT 7
 W08948
 ID W08948 standard; Protein; 107 AA.

AC W08948;

DT 18-SEP-1997 (first entry)

DE Kappa light chain variable region of 225RA antibody.

KW Kappa; light chain; reshaped; monoclonal; antibody; 225RA;
 KW human; epidermal growth factor; EGF; receptor; inhibition; growth;
 KW tumour; cell; late stage; prostatic; prostate; variable region;
 KW framework; complementarity determining region; CDR.

OS Homo sapiens.

PN Location/Qualifiers

FT Region 1..23 /label- framework_1

FT Region 24..34 /label- CDR_1

FT Region 35..49 /label- CDR_1

FT Region 50..56 /label- framework_2

FT Region 57..88 /label- CDR_2

FT Region 89..97 /label- framework_3

FT Region 98..107 /label- CDR_3

FT Region 108..127 /label- framework_4

PN W09640210-A1.

PD 19-DEC-1996.

XX PF 19-MAY-1999; 99WO-US11179.
 XX PR 20-MAY-1998; 98US-0086570.
 XX PA (TEIJ) TEIJIN LTD.
 XX PA (PROT-) PROTEIN DESIGN LABS INC.
 XX PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, CO MS, Vasques M;
 XX WP: 2000-086580/07.
 DR N-PSDB; 235244.
 DR
 PT Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli.
 XX
 PS Claim 12; Fig 2b; 59pp; English.
 XX
 CC This sequence represents a humanised light chain variable region of
 CC murine monoclonal antibody Vtm1-1 (MuVtm1-1), an antibody that
 CC specifically binds to the B subunit of verotoxin II (VT2). The
 CC invention relates to humanised antibodies against VT2 that are capable
 CC of neutralizing VT2 and/or VT2 variants. The humanised antibody is a
 CC humanized form of MuVtm1-1 comprising the complementarity determining
 CC regions of MuVtm1-1 and the heavy and light chain variable region
 CC frameworks from the human GF4 antibody heavy and light chain
 CC H30, H49 and H98 is occupied by the amino acid at the equivalent
 CC position of the MuVtm1-1 antibody heavy or light chain variable region
 CC framework. Such humanized antibodies have an affinity for VT2 that is
 CC 3-, 5 or 10-times that of MuVtm1-1. They are used for treating a
 CC patient suffering from, or at risk of, the toxic effects from VT2
 CC (claimed), especially for treating verotoxin producing Escherichia
 CC coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).
 CC
 XX Sequence 127 AA;
 SQ

Query Match 86.9%; Score 484; DB 21; Length 127;
 Best Local Similarity 88.8%; Pred. No. 7.6e-31;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTGSPATISLSPGERARISCOASQSIISNHLHWYQORPGAPRLIXYSOSISGIPA 60
 DB 21 EIVLTGSPATISLSPGERARISCOASQSIISNHLHWYQORPGAPRLIXYSOSISGIPA 80
 QY 61 RFSGSGSDFTLTITSSLEPEDFAVYTCQSGSWPHFTGGTKVEIK 107
 DB 81 RFSGSGSDFTLTITSSLEPEDFAVYTCQSGSWPHFTGGTKVEIK 127

RESULT 12
 R50192
 ID R50192 standard; Protein; 127 AA.
 XX
 AC R50192;
 XX
 DT 18-OCT-1994 (first entry)
 XX
 DE Light chain variable region C21-L3 of reshaped antibody.
 XX
 KW Antibody; heavy chain; light chain; variable region; therapy;
 KW constant region; prophylaxis; prevention; allergy; identification;
 KW allergic reaction; immunoglobulin; IGE; determination.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 44..54
 FT Binding-site /label- CDR 1.
 FT Binding-site 70..76
 FT Binding-site /label- CDR 2.
 FT Binding-site 109..117

FT
 XX
 XX EP589840-A. /label- CDR 3.
 XX
 XX 30-MAR-1994.
 XX
 XX 15-SEP-1993; 93EP-0810653.
 XX
 XX 24-SEP-1992; 92GB-0020228.
 XX 25-SEP-1992; 92US-0952802.
 XX
 XX (CIBA) CIBA GÉIGY AG.
 XX (TANO-) TANOX BIOSYSTEMS INC.
 XX
 PI Hardman N, Kolbinger F, Saldanha J;
 XX
 DR WP: 1994-103410/13.
 DR N-PSDB; 044716.
 DR
 XX
 PT New reshaped human monoclonal antibody specific for IGE - used
 PT for prophylaxis or treatment of allergic reactions or qualitative
 PT or quantitative determ. of IGE
 XX
 PS Example 2; Page 36; 68pp; English.
 XX
 CC Reshaped human monoclonal antibodies can be used in the prophylaxis
 CC and/or treatment of allergic reactions in humans. The monoclonal
 CC antibodies can also be used for the qualitative or quantitative
 CC determination of IGE and for the determination of surface IGE
 CC positive B cells. They can provide a long lasting therapeutic
 CC effect without inducing immunogenicity as foreign proteins. This
 CC sequence is a slightly modified version of C21-L1 described in
 CC R50187, having glutamic acid at position 1 of the mature protein
 CC instead of aspartic acid and valine at position 3 of the mature
 CC protein instead of leucine (positions 21 and 23 respectively of
 CC this sequence)
 CC
 XX Sequence 127 AA;
 SQ

Query Match 86.2%; Score 480; DB 15; Length 127;
 Best Local Similarity 85.0%; Pred. No. 1.5e-30;
 Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTGSPATISLSPGERARISCOASQSIISNHLHWYQORPGAPRLIXYSOSISGIPA 60
 DB 21 EIVLTGSPATISLSPGERARISCOASQSIISNHLHWYQORPGAPRLIXYSOSISGIPA 80
 QY 61 RFSGSGSDFTLTITSSLEPEDFAVYTCQSGSWPHFTGGTKVEIK 107
 DB 81 RFSGSGSDFTLTITSSLEPEDFAVYTCQSGSWPHFTGGTKVEIK 127

RESULT 13
 Y26982
 ID Y26982 standard; Protein; 127 AA.
 XX
 AC Y26982;
 XX
 DT 24-DEC-1999 (first entry)
 XX
 DE Light chain variable domain from antibody C21-L3.
 XX
 KW Diagnosis; IGE; immunoglobulin; body fluid; human; monoclonal antibody;
 KW binding affinity; mouse; CDR; complementarity determining region;
 KW allergy.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5958708-A.
 XX
 PD 28-SEP-1999.

XX 07-JUN-1995; 95US-0476176.
 PF 27-SEP-1993; 93US-0127721.
 PR 25-SEP-1992; 92US-0932802.
 XX (NOV) NOVARTIS CORP.
 PA (TANO-) TANOX BIOSYSTEMS INC.
 XX Saldanha J, Kolbinger F, Hardman N;
 DR WPI: 1999-570765/48.
 DR N-PSDB: 228548.
 XX new method for determining Ige levels in a sample
 PS Disclosure: Column 41-42; 19pp; English.
 CC The invention relates to a method of determining Ige levels in a body
 CC fluid sample, by contacting the sample with a reshaped human monoclonal
 CC antibody (RA) having a binding affinity about equal to that of the
 CC murine CDR-donor antibody TES-C21 produced by the cell line 11133.
 CC The antibodies are useful in the diagnosis, prophylaxis and treatment
 CC of allergy. This sequence represents the light chain variable domain
 CC from the reshaped human antibody C21-L3.
 XX
 SQ Sequence 127 AA;

Query Match 86.2%; Score 480; DB 20; Length 127;
 Best Local Similarity 85.0%; Pred. No. 1.5e-30;
 Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 EIVLQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGAPRLILYXSQISGIPA 60
 DB 21 elvltqspqtlslspgeratlsqrasqslglnlhwypqgqaprlilkyaseslsqips 80
 QY 61 RFGSGSGTDFTLTISLSEPEDFAVYICQSGSWPHFEGGTKEIK 107
 DB 81 rfsqsgsgtdftltisrlepedfavyicqsgswphtfsggtkveik 127

RESULT 14
 R37612
 ID R37612 standard; Protein; 107 AA.
 AC R37612;
 DT 13-OCT-1993 (first entry)
 DE hIL2R Ab L chain V region.
 XX
 KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 KW human; Interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid; heavy; H; light; L.
 OS Mus musculus/Homo sapiens.
 XX
 PN WO9311238-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; 92MO-JP01583.
 PR 06-DEC-1991; 91JP-0323319.
 XX (BIOT) BIOTEST PHARMA GMBH.
 PA (INNO-) INNOTHERAPIE LAB.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 XX Gomi H, Nakatani T, Noguchi H, Wajdenes J;
 DR

DR WPI: 1993-197057/24.
 DR N-PSDB: Q43245.
 XX Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor
 XX
 PS Claim 2; Fig 5; 62pp; English.
 CC The sequences given in R37611-12 represent the heavy (H) and light (L)
 CC chain variable (V) regions of a humanised antibody (Ab) which binds
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). The
 CC complementarity-determining regions (CDRs) of these V regions were
 CC derived from the murine anti-human IL-2 receptor monoclonal Ab (Mab)
 CC B-B10 (see also R37599-04). This Mab is antagonistic to the binding
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
 CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.
 XX
 SQ Sequence 107 AA;

Query Match 85.8%; Score 478; DB 14; Length 107;
 Best Local Similarity 86.0%; Pred. No. 1.9e-30;
 Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 1 EIVLQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGAPRLILYXSQISGIPA 60
 DB 1 elvltqspqtlslspgeratlsqrasqslglnlhwypqgqaprlilkyaseslsqips 60
 QY 61 RFGSGSGTDFTLTISLSEPEDFAVYICQSGSWPHFEGGTKEIK 107
 DB 61 rfsqsgsgtdftltisrlepedfavyicqsgswphtfsggtkveik 107

RESULT 15
 Y70604
 ID Y70604 standard; Protein; 107 AA.
 AC Y70604;
 DT 18-JUL-2000 (first entry)
 DE V kappa region of humanised antibody Hu-901.
 XX
 KW Humanised antibody-901; Hu-901; V kappa; kappa chain variable region;
 KW anti-IGF; anti-immunoglobulin E; monoclonal antibody; hybridoma TES-C21;
 KW recombinant adenovirus vector; anti-IGF antibody; gene therapy; scfv;
 KW single chain variable fragment; allergy; anti-allergic.
 OS Homo sapiens.
 XX
 PN WO200015260-A1.
 PD 23-MAR-2000.
 PF 16-SEP-1999; 99WO-US21646.
 PR 16-SEP-1998; 98US-0100639.
 XX (TANO-) TANOX INC.
 PA Llou RS, Thomas D;
 XX WPI: 2000-271264/23.
 DR N-PSDB: 252078.

XX New nucleic acids encoding anti-IgE antibodies such as Hu-901 or their
 PT fragments, useful in the gene therapy of allergic diseases -
 XX
 PS Disclosure; Page 47; 52pp; English.

CC The present protein sequence is the Ykappa (kappa chain variable region)
 CC of the humanised antibody Hu-901. This is an exemplary anti-IgE (anti-
 CC -immunoglobulin E) monoclonal antibody produced by hybridoma TES-C21. The
 CC heavy and light chains are obtained through RT-PCR using the RNA from the
 CC transfectoma cell line producing the chimeric antibody. Humanised
 CC anti-IgE genes are incorporated in the genome of a recombinant adenovirus
 CC vector as an independent transcriptional unit, and packaged into
 CC infectious virus particles. Upon infection of host, the recombinant
 CC adenovirus vector will direct the production of either intact anti-IgE
 CC antibody or an scFv fragment in the serum, which will bind free
 CC circulating IgE, resulting in the reduction of free serum IgE. The
 CC binding of the antibody or fragment to IgE-bearing B cells may lower IgE
 CC levels by down-regulating IgE production by these B cells. These methods
 CC are useful in the gene therapy of allergic diseases.

XX
 SQ Sequence 107 AA;

Query Match 85.1%; Score 474; DB 21; Length 107;
 Best Local Similarity 83.2%; Pred. No. 3.8e-30;
 Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTSPATLSLSPERATLSQASQSTISNHLHWYQORPGAPRLIYRSQSTIGIPA 60
 DB 1 dilltspptlslspgratlsrctasgsigtlnhwqkpgqgprlllkyseslsigls 60
 QY 61 RFGSGSGTDFITITISLEPEDFAVYVCOOSGSMPTFGGTFVEIK 107
 DB 61 rfsqsgsgtdftltlsrlepedfamyvqgsdswptlfgqgkveik 107

Search completed: February 13, 2001, 09:03:48
 Job time: 57 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:03:16 : Search time 18.5 seconds

(without alignments)
103.860 Million cell updates/sec

Title: US-08-790-540a-4

Perfect score: 357

Sequence: 1 EIVLTQSPARLSLSPGERAT.....COQSGSWPHTFGGTGKVEIK 107

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506	90.8	107	1	US-07-634-278-63 Sequence 63, Appl
2	506	90.8	107	1	US-07-634-278-87 Sequence 87, Appl
3	506	90.8	107	1	US-08-477-728-63 Sequence 63, Appl
4	506	90.8	107	1	US-08-477-728-87 Sequence 87, Appl
5	506	90.8	107	1	US-08-474-040-63 Sequence 63, Appl
6	506	90.8	107	1	US-08-474-040-87 Sequence 87, Appl
7	506	90.8	107	1	US-08-487-200-67 Sequence 67, Appl
8	506	90.8	107	1	US-08-487-200-87 Sequence 87, Appl
9	480	86.2	127	2	US-08-476-176B-10 Sequence 10, Appl
10	480	86.2	127	3	US-08-485-246A-10 Sequence 10, Appl
11	480	86.2	127	3	US-08-485-246A-10 Sequence 10, Appl
12	474	85.1	127	2	US-08-476-176B-6 Sequence 6, Appl
13	474	85.1	127	3	US-08-127-721A-6 Sequence 6, Appl
14	474	85.1	127	3	US-08-485-246A-6 Sequence 6, Appl
15	473	84.9	107	2	US-08-232-081B-9 Sequence 9, Appl
16	471	84.6	127	3	US-08-476-176B-8 Sequence 8, Appl
17	471	84.6	127	3	US-08-127-721A-8 Sequence 8, Appl
18	471	84.6	127	3	US-08-485-246A-8 Sequence 8, Appl
19	449.5	80.7	107	3	US-08-783-853A-44 Sequence 44, Appl
20	441	79.2	107	1	US-07-634-278-62 Sequence 62, Appl
21	441	79.2	107	1	US-08-477-728-62 Sequence 62, Appl
22	441	79.2	107	1	US-08-474-040-62 Sequence 62, Appl
23	441	79.2	107	1	US-08-487-200-62 Sequence 62, Appl
24	441	79.2	127	1	US-07-634-278-83 Sequence 83, Appl
25	441	79.2	127	1	US-08-477-728-83 Sequence 83, Appl
26	441	79.2	127	1	US-08-474-040-83 Sequence 83, Appl
27	441	79.2	127	1	US-08-487-200-83 Sequence 83, Appl
28	438	78.6	127	1	US-08-436-463-4 Sequence 4, Appl

29	434	77.9	107	1	US-08-436-463-20 Sequence 20, Appl
30	434	77.9	109	1	US-07-942-245-4 Sequence 4, Appl
31	432.5	77.6	107	3	US-08-783-853A-57 Sequence 57, Appl
32	431	77.4	107	1	US-08-107-669D-1 Sequence 1, Appl
33	431	77.4	107	1	US-08-472-788A-1 Sequence 1, Appl
34	431	77.4	107	2	US-08-477-531B-1 Sequence 1, Appl
35	431	77.4	107	2	US-08-082-842A-1 Sequence 1, Appl
36	430.5	77.3	108	2	US-08-232-081B-42 Sequence 42, Appl
37	430	77.2	111	1	US-07-634-278-47 Sequence 47, Appl
38	430	77.2	111	1	US-08-477-728-47 Sequence 47, Appl
39	430	77.2	111	1	US-08-474-040-47 Sequence 47, Appl
40	430	77.2	111	1	US-08-487-200-47 Sequence 47, Appl
41	429.5	77.1	107	3	US-08-783-853A-62 Sequence 62, Appl
42	427	76.7	107	1	US-08-107-669D-14 Sequence 14, Appl
43	427	76.7	107	1	US-08-472-788A-14 Sequence 14, Appl
44	427	76.7	107	2	US-08-477-531B-14 Sequence 14, Appl
45	427	76.7	107	2	US-08-082-842A-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-63 : Application US/07634278
Sequence 63, Appl
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: ODEEN, Gary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLF, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPA 60
1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPA 60
Db 1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPD 60

QY 61 RSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107
61 RSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107
Db 61 RSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107

RESULT 2

US-07-634-278-87
Sequence 87, Application US/07634278
Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634, 278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 90.8%; Score 506; DB 1; Length 107;

Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPA 60
1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPA 60
Db 1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPD 60

QY 61 RSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107
61 RSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107
Db 61 RSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107

RESULT 3

US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPA 60
1 EIVLTOSPATLSLSPGERATLSCQASOSISNNLHWYQORPGAPRLIXRSQISGIPA 60

DB 1 EIVLTQSPGTLISLSPGERATLISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
QY 61 RFGSGSGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107
DB 61 RFGSGSGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107

RESULT 4

US-08-477-728-87
Sequence 87, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATISLSPGERATLISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
DB 1 EIVLTQSPGTLISLSPGERATLISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
QY 61 RFGSGSGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107
DB 61 RFGSGSGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107

RESULT 5
US-08-474-040-63
Sequence 63, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATISLSPGERATLISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
DB 1 EIVLTQSPGTLISLSPGERATLISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
QY 61 RFGSGSGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107
DB 61 RFGSGSGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107

RESULT 6

US-08-474-040-87
Sequence 87, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

DB 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQKPGAPRLILXYSSQISGIPA 60
1 EIVLTQSPETLSLSPGERATLSCRASQSIHNLHWYQKPGAPRLILXYSSQISGIPD 60

QY 61 RSSGSGSGTDFTLTISLEPEDFAVYYCOQSGSNPHTFGGKTVK 107
1 RSSGSGSGTDFTLTISLEPEDFAVYYCOQSGSNPHTFGGKTVK 107

DB 61 RSSGSGSGTDFTLTISLEPEDFAVYYCOQSGSNPHTFGGKTVK 107

RESULT 7
US-08-487-200-63
Sequence 63, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

DB 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQKPGAPRLILXYSSQISGIPA 60
1 EIVLTQSPETLSLSPGERATLSCRASQSIHNLHWYQKPGAPRLILXYSSQISGIPD 60

QY 61 RSSGSGSGTDFTLTISLEPEDFAVYYCOQSGSNPHTFGGKTVK 107
1 RSSGSGSGTDFTLTISLEPEDFAVYYCOQSGSNPHTFGGKTVK 107

DB 61 RSSGSGSGTDFTLTISLEPEDFAVYYCOQSGSNPHTFGGKTVK 107

RESULT 8
US-08-487-200-87
Sequence 87, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELING, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,200
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 87:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-487-200-87

Query Match 90.8%; Score 506; DB 1; Length 107;
 Best Local Similarity 90.7%; Pred. No. 9,1e-41;
 Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EIVLTOSPATSLSPGERATISCOASOSISNHLHWYQORPGQAPRLIXYRSOSISGIPA 60
 DB 1 EIVLTOSPATSLSPGERATISCOASOSISNHLHWYQORPGQAPRLIXYRSOSISGIPD 60
 QY 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKYEIK 107
 DB 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKYEIK 107
 RESULT 9
 US-08-476-176B-10
 Sequence 10, Application US/08476176B
 Patent No. 5958708
 GENERAL INFORMATION:
 APPLICANT: Hardman, No. 5958708man
 APPLICANT: Kolbinger, Frank
 APPLICANT: Saldanha, Jose

TITLE OF INVENTION: Reshaped monoclonal antibodies against an
 TITLE OF INVENTION: Immunoglobulin isotype
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5958708artls Patent Department
 STREET: 59 Route 10
 CITY: East Hanover
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07936-1080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476,176B
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/127,721
 FILING DATE: 27-SEPTEMBER-1993
 APPLICATION NUMBER: US 07/952,802
 FILING DATE: 25-SEPTEMBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5958708ak, Henry P.
 REGISTRATION NUMBER: 33,200
 REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 277-5110
 TELEFAX: (908) 277-4306
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 127 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-476-176B-10

Query Match 86.2%; Score 480; DB 2; Length 127;
 Best Local Similarity 85.0%; Pred. No. 2,9e-38;
 Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 EIVLTOSPATSLSPGERATISCOASOSISNHLHWYQORPGQAPRLIXYRSOSISGIPA 60
 DB 21 EIVLTOSPATSLSPGERATISCOASOSISNHLHWYQORPGQAPRLIXYRSOSISGIPS 80
 QY 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKYEIK 107
 DB 81 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKYEIK 127

RESULT 10
 US-08-127-721A-10
 Sequence 10, Application US/08127721A
 Patent No. 6066718
 GENERAL INFORMATION:
 APPLICANT: Hardman, No. 6066718man
 APPLICANT: Kolbinger, Frank
 APPLICANT: Saldanha, Jose
 TITLE OF INVENTION: Reshaped monoclonal antibodies against an
 TITLE OF INVENTION: Immunoglobulin isotype
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6066718artls Patent and Trademark Department
 STREET: 59 Route 10
 CITY: East Hanover
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07936-1080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6065718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-127-721A-10

Query Match 86.2%; Score 480; DB 3; Length 127;
Best Local Similarity 85.0%; Pred. No. 2.9e-38;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQGISNHLHWYQORPGQAPRLLIYRSQISIGIPA 60
DB 21 EIVLTQSPETLSLSPGERATLSCRASQSIGTNIHWYQORPGQAPRLLIYKASISIGIPS 80
QY 61 RSSGSGGTDFTLTISLPEPEFANYVYCOQSDSWPTTFGGGTKEIK 107
DB 81 RSSGSGGTDFTLTISLPEPEFANYVYCOQSDSWPTTFGGGTKEIK 127

RESULT 11
US-08-485-246A-10
Sequence 10, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 6072035artlis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.

REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-246A-10

Query Match 86.2%; Score 480; DB 3; Length 127;
Best Local Similarity 85.0%; Pred. No. 2.9e-38;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQGISNHLHWYQORPGQAPRLLIYRSQISIGIPA 60
DB 21 EIVLTQSPETLSLSPGERATLSCRASQSIGTNIHWYQORPGQAPRLLIYKASISIGIPS 80
QY 61 RSSGSGGTDFTLTISLPEPEFANYVYCOQSDSWPTTFGGGTKEIK 107
DB 81 RSSGSGGTDFTLTISLPEPEFANYVYCOQSDSWPTTFGGGTKEIK 127

RESULT 12
US-08-476-176B-6
Sequence 6, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 5958708artlis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-176B-6

GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,081B
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: SVENSSON, LEONARD R
 REGISTRATION NUMBER: 30,330
 REFERENCE/DOCKET NUMBER: 20-3484
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-232-081B-9

Query Match 84.9% Score 473; DB: 2; Length 107;
 Best Local Similarity 85.8% Pred No. 1.1e-37;
 Matches 91; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSIHNLHWYQKRGQAPRLILYRSQISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCAQSQSIHNLHWYQKRGQAPRLILYRSQISGIPA 60
 QY 61 RFGSGSGTDFLTITSSLEPEDPAVYCCQSSGSMPTFGGKVEI 106
 DB 61 RFGSGSGTDFLTITSSLEPEDPAVYCCQSSGSMPTFGGKVEI 106

Search completed: February 13, 2001, 09:03:17
 Job time: 25 sec